

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 300

TO: Ralph J Gitomer Location: 3d65 / 3c18

Art Unit: 1655

Friday, September 16, 2005

Case Serial Number: 10/650482

From: Noble Jarrell

Location: Biotech-Chem Library

Rem 1B71

Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes		
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Scientific and Technical Information Center

SEARCH REQUEST FORM

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Direct Submission
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morernan, K.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lulyk, S.W.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and mouse cDNA sequences
D. A., Anderson, B. M. Schein, J. S., Maria, M. J., Schein, J. Schaus, M. J., Schein, J. S., Maria, M. J., Schaus, M. J., Schein, J. S., Maria, M. J., Schaus, M. J., Schein, J. S., Maria, M. J., Schaus, M. J., Schein, J. Schaus, M. J., Schein, J. Schaus, M. J., Schein, J. Schaus, M. J., Schaus, M. J., Schaus, M. J., Schaus, M. J., Schein, J. Schaus, M. J., Schaus, M. J., Schaus, M. J., Schaus, M. Schein, J. Schaus, M. J., Schaus, M. J., Schaus, M. J., Schein, J. Schaus, M. J., Schaus, M. Schaus, M. Schaus, M. Schaus, M. J., Schaus, M. Sch
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                                                                                                                                                                       PRI 12-OCT-2004
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Web site: http://www.nisc.nnh.gov/
Rotact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 5264)
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                                                                                                                                                     HCU65280 5264 bp mRNA linear PRI 12-OCT
HOMO sapiens CDNA clone MGC:74824 IMAGE:6172811, complete cds.
BC065280
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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SGNPTLLSSAQPETRYSYWTKLLSQLLAPLPCILQKVLIWSQLFGGWFPTRWLDFAGV
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ASWQGCPPLSTEGLPEIHHLRWKRLEFLQQASKQDLPTPDQDNGYHSLEEBEHSLLRM
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DSEKDLSGKSDLENSSQSGSLPETPEHSSGEEDDWESSADEABSLLKUNFEUPEDPY
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RDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDA
IGYCLTFEHRERMFNRLQGTCFKGLNVLKQC"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="MGC:74824 IMAGE:6172811"
/tissue_type="Byc retinoblastoma"
/clone_lib="NHH MGC_67"
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Pred. No. 0;
0; Mismatches
                                                                                            'note="Vector: pCMV-SPORT6"
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Pred. No. 0;
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.3"
                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
1 (bases 1 to 167079)
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99.8%;
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                                              GGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAG 1886
                                                                      GGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAG 1860
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_alegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RRP11-739N20 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                          2821 CATTTTGCACTTTCAAAACTTATTTTCTTGGAAAACAATATTTATAGGGCTTAAAGGCCCA 2880
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Catarrhini, Hominidae, Homo.
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     CATTTTGCACTTTCAAAACTTATTTTCTTGGAAAACAATATTTATAGGGCTTAAAAGCCCA
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Grouse L.H., Derge, J.G.,
ner, L., Shenmen, C.M., Schuler, G.D.,
w.K.H., Schaefer, C.F., Bhat, N.K.,
w.Max, S. I., Wang, J., Hsieh, F.,
er, A.A., Rubin, G.M., Hong, L.,
do, M.F., Casavant, T.L.,
do, M.F., Casavant, T.L.,
Loquellano, N.A., Peters, G.J.,
k.S.A., McEwan, P.J.,
k.S.A., McEwan, P.J.,
atne, P.H., Richards, S.,
day, L.J., Hulyk, S.W.,
yen, B.J., Lu, X., Gibbs, R.A.,
madan, A. Rodrigues, S.,
madan, A. Rodrigues, S.,
noung, A.C., Shevchenko, Y.,
ouchman, J.W., Green, E.D.,
imwood, J., Schmutz, J., Myers, R.M.,
S.J. and Marra, M.A.
S.J. and Marra, M.A.
GGCCATTTCTGAGTGTCACACCTTACT 2220
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Centre,
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GGCTCCTGGTTCCGGCTGCCC---TTCCTTCGGCGATCGCACGCCTGCTCTTCGGAGTTC
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                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 126 Row: n Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27597066. Location/Qualifiers
  Prabhu, Parvaneh Saeedi, Jacqueline
Smith, Lorraine Spence, Jeff Stott,
Nataesja van den Bosch, Jill Vardy,
Marco Marra.
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/organisme="Mus musculus"

/mol_type="mistan"

/strain="C57BL/6"

/db_xref="teaxon:10090"

/clone="MGC:66517 IMAGE:6830215"

/clone_Iib="NH BMAP FOO"

/lab_host="DH10B"

/note="Vector: pYX-ASC"
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-xref="MGI:2444211"
  Ness, Pawan Pandoh, Anna-Liisa
Schain, Duane Smallus, Michael
Michael Thorne, Miranada Tsai,
George Yang, Scott Zuyderduyn,
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der, E., Abraham, H., Allen, N., stien, V., Beda, F., A., Burkett, G., A., Burkett, G., Colangelo, M., Collins, S., Dewar, K., Diaz, J.S., ette, M., Graham, L., Karatas, D., ette, M., Graham, L., Karatas, R., Karnar, T., Karatas, R., Macdonald, P., Marquis, N., Macdonald, P., Marquis, N., Manda, C., Mlenga, V., Morrow, J., Sonnor, T., O'Donnell, P., Spencer, B., carson, K., Pierre, N., ley, R., Rogov, P., Rothman, D., P., Spencer, B., camanian, A., Talamas, J., fravers, M., Trigilio, J., Ye, W.J., ody, M.
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TCAGGTTTGAAGCCAGCCCTGA 2734
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84G5
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NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                              Insert size: 163433; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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FEATURES Source

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All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                      153103 GCCTTCTCTGGCCATCATACCTTACTTGTAAGGCCCAGCTGTTAGAGAGCCAAGAA 153162
                                      153163 GATAATTGTCCAGGCTGTGGGTGAGGCTCTTGCTGGAAGATACACCCCATATC 153222
                                                                                                                            Rattus norvegicus clone CH230-194B23, *** SEQUENCING IN PROGRESS
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                  AC128396.4 GI:23322373
HTG; HTGS PHASE1; HTGS DRAPT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                153223 AAGAGAAAAAGGITTGTTCCCTTTTACATG 153253
                                                                2315 AAAAGAAAAAGGTAACCTTCCTTGAAGAAG 2345
                                                                                                                                                                                                                                   (bases 1 to 200490)
                                                                                                                                                                                                                            Rattus.
                                                                                                             RESULT 10
AC128396/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                       DEFINITION
                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                   REFERENCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                          Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases I to 200490)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (126-58P-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
On Sep 26, 2002 this sequence version replaced gi:22771040.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 111649 bases at least Q40
Consensus quality: 118620 bases at least Q30
Consensus quality: 118824 bases at least Q20
Estimated insert size: 161200; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21048: contig of 21048 bp in length 21148: gap of unknown length 108746: contig of 87598 bp in length 10846: gap of unknown length 161819: contig of 52973 bp in length 161819: gap of unknown length 17640: gap of unknown length 176740: gap of unknown length 18747: gap of unknown length 18747: gap of unknown length 18747: gap of unknown length 200490: contig of 13043 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
Center code: BCM
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/organism="Rattus norvegicus"
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misc_feature 2114923404 misc_feature 7004e="wgs_contig" misc_feature 7009e="wgs_contig"	Query Match ATTITICAGGETTCACCGCACCGCACCCCACCCCACCCCACCCCTACCGGTTCCCCTTCCCGCTTCCCTTTCTTT

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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
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Unpublished
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Direct Submission
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayogi, A., Baca, E., Baden, H., Balakin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, B., Brown, M., Cardenso, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Dinh, H., Divys, K., Drayle, M., Escotto, M., Evgene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gebregeorgis, B., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Gancia, A., Garner, T., Garcia, A., Garner, T., Gebregeorgis, B., Garcia, A., Hanliton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hanles, S., Hlanes, S., Hlandin, S., Home, J., Idlebird, D., Jackson, A.,
   195792 TGAATCAGACAGGGAACAAGACTCCGAAGGGCTTCACCTTTGGAACTCTTTCTACAGTGT 195733
                                                                                                                    195732 AGATCCTTACAACCCCCAGAACTTTACAGCCACAATTCAGACTGCTGCCAGAATTGCCCC 195673
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Rattus norvegicus clone CH230-191M14, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                             1858 AGATCCTTATAATCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCC
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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SUDMILLEAU (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:25089918.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.mc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold') within each contig-scaffold') within each contige seguence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table. Jackson, J., Jacob, J., Jang, H., Johnson, B., Johnson, K., Jackson, J., Jackson, J., Jacob, J., Jang, H., Johnson, B., Johnson, K., Koyar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewai, L., Liu, W., Liu, Y., London, R., Lu, X., Ma, J., Lorensuhewai, J., Loudon, P., Longacre, S., May, J., Martin, K., Martinez, E., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martinez, E., Mangum, A., Mantin, B., Mapua, P., Martin, K., Martinez, E., Milosavijevic, A., Mine, G., Minja, E., Montemayor, J., Moore, S., Milosavijevic, A., Mine, G., Minja, E., Montemayor, J., Moore, S., Milosavijevic, A., Morris, S., Munidasa, M., Norris, K., Martin, K., Norris, S., Munidasa, M., Norris, K., Martin, N., Nguyen, N., Norris, S., Parks, K., Pasteris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Pauk, K., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perey, C., D., Frimus, E., Pu, L.-L., Plopper, F., Poindexter, A., Perey, C., D., Frimus, E., Pu, L.-L., Rives, C., Rodkey, T., Rachilly, M., Ren, Y., Rose, M., Rose, R., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Riggs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvartsbeyn, A., Sisson, I., Stter, C.D., Smajs, D., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Vara, K., Warren, J., Warren, R., Warts, M., Warren, R., Warren, S., Warken, S., Warken, J., Warren, R., Warlen, W., Warren, J., Warren, R., Warren, S., Warken, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Dunn, D., von Niederhausern, A., Waiss, R., Submitted (07-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 227054)

Rat Genome Sequencing Consortium.

Direct Submission Assembly program: Atlas 3.0;
Consensus quality: 214697 bases at least Q40
Consensus quality: 21752 bases at least Q30
Consensus quality: 219170 bases at least Q30
Estimated insert size: 224268; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor College of Medicine Center code: BCM Contact: hgsc-help@bcm.tmc.edu
------ Broject Information
Center project name: GIJO
Center clone name: CH230-191M14 ------ Genome Center (bases 1 to 227054)

* NOTE: Estimated insert size may differ from sequence length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 ACTGCTCTCCCAGCTCCTTGCGCCGCTCCCCGGATTGCTTCAGAAGGTGCTAATTTGGAG
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                                                                                                                                                                                                                                                                                                    Gaps
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_danors: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                Length 227054;
                                                                                                                                                                                                                                                                                                    92;
                                                                                                       1 35084: contig of 35084 bp in length
35184: gap of unknown length
15 224939: contig of 189755 bp in length
10 225039: gap of unknown length
10 227054: contig of 2015 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                              Score 1137.4; DB 2; Length
Pred. No. 5.4e-296;
0; Mismatches 586; Indels
                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                     /clone="CH230-191M14"
145242. .147317
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                                                                                                                                                                                                                                                                              38.7%;
llarity 71.6%;
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GTTGCTGCCCGGTAGTCTTCAAACCGGTCTAGTCTCCCACCGAGAACTTGGCTCTTCATC 152014
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                                                                                                                                                                                                                                                                                               TCAACAGGCTAACAAGGGGCAAGATTTACCCACCCCTGACCAGGATAATGGCTACCACAG
                                                                                                                                                                                                 GGAGGGGATCCACTGGCAATACTCGCCCCCAGACCTAAAATTGGAGCTTAAGGCCAAGGG
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                                                                                                                                                                      TTCGCTGCAGCTCGAC - - TCCTCAGACCCCTCGGTCACCCAGTCCCCTTGATTGGCTAGA
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* NOTE: Bstimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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Anlen, C., Allen, H., Alabrooke, S., Amin, A., Angulano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

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Cardenas, V., Carter, K., Cavacos, I., Ceasar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

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Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Dermo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

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Fernandez, S., Finley, M., Flaggy, N., Foster, M., Garrer, M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
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                                                                                                                                                    151284 TGAATCAGACAGGGAACAAGACTCCGAAGGGCTTCACCTTTGGAACTCTTTCTACAGTGT 151225
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                                                                          1798 AGACTCAGACCTTGAACAAGACCCTGAAGGCCTTCACCTTTGGAACTCTTTCTGCAGTGT 1857
                                                                                                                                                                                                                                  1958 AGATCCTTATAATCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCC 1917
                                                                                                                                                                                                                                                                                                                                                                                           1918 TGAAGAGCCTTCTGATTCAGAGGATTTGTCTGGCAAGTCTGATCTAGAGAATTCCTC 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2038 ATCTAGTGCAGATGAAGCAGAGAGTCTCAAACTGTGGAACTCGTTCTGTAATTCTGATGA 2097
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Mammalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150756 TITACATGACTTATAATTTGTTGTTTTTTGATATGGTTACAGTAGAAGA 150708
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Rattus norvegicus (Norway rat)
Rattus norvegicus
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Gunaratne, Y., Haaland, W., Hamil, C., Hamilton, K., Harvey, Y., Havlak, P., Hadan, C., Hamilton, K., Harvey, Y., Havlak, P., Hadens, M., Hodgson, M., Hogues, M., Howels, M., Hodgson, M., Hogues, M., Howels, M., Hollins, B., Howells, S., Hulyk, S., Hung, J., Johnson, R., Johnson, R., Jackson, L., Jacob, L., Jacop, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kovis, C., Liu, M., Liu, M., Lewis, L., Lougacre, S., Lopez, J., Lorensuhewa, L., Loulesged, H., Lozado, R.J., Lux, K., Manjou, A., Mahindarlen, M., Mahmoud, M., Martin, K., Martin, R., Martin, K., Martin, R., Manjou, B., Mandarlen, M., Mahmoud, M., Martin, R., Martin, K., Martin, R., Martin, R., Martin, R., Martin, M., Morris, S., Morgan, M., Morris, K., Morris, S., Morgan, M., Morris, K., Morris, S., Morgan, M., Morris, K., Morris, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plankervis, C., Newton, G., Olaripunasgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plankervis, C., Mula, E., Morris, S., Riggs, F., Reilly, B., Reilly, M., Ren, Y., Rose, R., Ruiz, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, R., Ruiz, S., Riggs, F., Rives, C., Soret, G., Shateman, S., Shen, H., Short, Y., Shvattsbern, S., Stote, G., Shateman, S., Shen, H., Short, Y., Stote, C.D., Smajs, D., Shetty, J., Walders, R., Yalos, S., Umns, J., Wang, J., Walder, B., Walder, B., Walder, B., Wang, C., Walder, B., Walder, Submitted (12.52P-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houseron, TX 77030, USB.

Baylor Plaza, Houseron, TX 77030, USB.

The Bequence in this assembly is a combination of BAC based reads and whole genome shotgun sequence reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table. Direct Submission
Submitted (10-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to -248458)
Rat Genome Sequencing Consortium.
Direct Submission Quality coverage: 5x in Q20 bases; sum-of-contigs estimation Center clone name: CH230-101J7
Assembly Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 231489 bases at least Q40
Consensus quality: 232351 bases at least Q30
Consensus quality: 232940 bases at least Q30
Estimated insert size: 249328; sum-of-contigs estimation Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center project name: GNVL Genome Center

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ACTGATAGATTATATTTTGGGAGGTGCAFTGGAGGAGCTGGAAACAAGTTCTGATCCAGA 1737
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  4686 TCTAAGAGCTTTGAGAGGACGGAGGAATCAGCCGCTCCCACAGTGCAGAAATCTTTGAA
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* NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 244458: contig of 248458 bp in length.
Location/Qualifiers
| 1 248458: contig of 248458 bp in length.
| 1 248458: contig of 248458 bp in length.
| 2 248458: contig of 248458 bp in length.
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Pred. No. 5.4e-296;
0; Mismatches 586;
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complement(247315. .248169)
/note="clone boundary
clone end:Sp6
site:EcoRI
end_sequence:BH312303"
                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-101J7"
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/note="clone_boundary
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Best Local Similarity 71.6%;
Matches 1711; Conservative
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Rattus norvegicus clone CH230-146P11, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                                                                                                                                                                      5715 rgaarcagacagggaacaagacrccgaaggcrrrcaccrrrrggaacrcrrrrchacagrgr 5774
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5595 ACTGATAGATTATATTTTGGGAGGAGCCTCCAGTGACTTGGACACCAGCTCCGATTCTGA 5654
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                         5655 AAGTGAGGATGGGAACCTGAGGATGATGGTTTTGATAGTGATGCTCCTATC
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULITOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Fernandez, S., Finley, M., Eugens, C., Byans, C., A., Falls, J., Fanlor, Fernandez, S., Finley, M., Eugens, C., M., Gabisi, A., Garlez, R., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, A., Garcia, M., Guerza, M., Gubregeorgis, B., Gaer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunzatne, P., Haaland, W., Hamill, Cn., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Holles, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, K., Johnson, K., Johnson, S., Koper, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorlesged, H., Lorado, R., Malloy, K., Mangum, A., Mahulawa, L., Mahudartne, M., Mahundartne, S., McLeod, M.P., Modeill, T.Z., Menenn, E., Mangum, A., Mangum, B., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Mal, D., Nawcon, M., Norris, S., Munidasa, M., Murphy, M., Nair, L., Pastenne, S., Pasternak, S., Paul, H., Perze, M., Perze, L., Pfannkoch, C., Reigh, R., Perze, C., Rodkey, T., Roge, M., Rose, M., Rose, R., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Jose, Shetty, J., Shvattsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Shvattsbeyn, A., Strong, R., Walzer, M., Trejos, Z., Usman, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Waldron, L., Walker, B., Waldron, L., Walker, B., Walder, M., Walse, R., Walth, D., Walder, M., Walse, R., Malton, R., Walth, D., Walder, M., Walse, R., Malton, R., Walth, D., Walder, M., Walse, R., Smith, D., Naith, D., Walder, M., Walse, R., Smith, D., Waller, M., Walse, R., Smith, D., Waller, M., Walse, R., Malton, R., Walth, R., Smith, D., Waller, M., Walse, R., Malton, R., Malton, R., Malton, R., Malton, R., Malton, R., Malton, R., Smith, D., Walth, R., Walth, M., Walt
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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23194778.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Direct Submission
Submitsed (02-Mar-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 212261)
Rat Genome Sequencing Consortium.
Falls, T., Fan, G.,
    Escotto, M., Eugene, C., Evans, C.A.,
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                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646
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Assembly program: Phrap; version 0.990329
Consensus quality: 199836 bases at least Q40
Consensus quality: 201017 bases at least Q30
Consensus quality: 201015 bases at least Q30
Consensus quality: 202375 bases at least Q20
Estimated insert size: 203079; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140716 TGCTGCCCTTCCTTAG---GGCGATCACACGCCTGCACTTCTGAGTTCCCGAAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140875 CTGCTTATTTGGAGTCAGCTTTTCGGTGGCATGATTCTGACCAGATGGCTATACTTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40995 GCAGAAATCTTTGAGTTCTCTGCGGCTGGATTTTTCTTCGGAAGACTTGGCTGTCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140598 CTTCGCTCTGATGCCGCTGAGCTCCGTACTCCTGCCCGTGAAGTTGCCAAG-GAAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGCCACCCTTTTTCCCTCGGCGATCGCAGCAGGCTCTTCTAAGTTCCCGACGCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCCGGAAAACTCCGGGAACCCCACACTGCTTTCCTCTGCCCAGCCCGAGACTCGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140773 TCTCAACCAAATCTCGAGGA-----CTCTGCCTGGTCCGAGCCTCAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTACTGGACGAAACTGCTCTCCCAGCTCCTTGCGCCCGCTCCCCGGATTGCTTCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140818 AGGTACTGGACCAAATTGCATTCCCAGTTCCTTG---CTCTCCCTAGCTTGCTCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               647 GTGCTAATTTTGGAGCCAACTTTTCGGTGGAATGTTTCCGACCAGATGGCTAGATTTTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGTCTACAGGCGCCCTGAGGCCCCTGAAGGGACGGGA - GAAACCAGCCGCCCCCACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140935 GCAAGTTACAGCTCCCTGCGAGCTTTGAGAGGACCGGAGGAAATCAGCCGCTCCCACGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                        11068: contig of 11068 bp in length
11168: gap of unknown length
212261: contig of 201093 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%; Score 1120.2; DB 2;
larity 71.6%; Pred. No. 2.4e-291;
Conservative 0; Mismatches 603;

    .212261
    /organism="Rattus norvegicus"

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/db_xref="taxon:10116"
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                                                        141174 gereregegagragarrecrececerecretreaacceareragrereceaeaaa
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                                                                                                                          ACTIGGCICTICGCCCTCTGGGCCTCTAAACATTCAACGCATAGACAATTTCAGTGTGG
                                                                                                                                                                                                                                                     1063 ATCCTATTTGCTGAACCCTTCCTACCTGGACTGCTTTCCTAGGCTAGAAGTCAGCTATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus clone CH230-3B24, *** SEQUENCING IN PROGRESS ***, AC094236
                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCAAAGGACCATGGGAAGAATTTGCAAGGGATGGATGCAGGTTCCAGAAACGAATTCAA 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2498 AGACTCCAGGGAACAIGCTTCAAAGGACTTAATGTTCTCAAGCAATGTTGAGTTG-GCAG 2556
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GGAAGATGACTGGGAATCTAGTGCAGATGAAGCAGAGAGTCTCAAACTGTGGAACTCATT 2082
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
                      142211 GGAGGATGACTGGGAACCTAGTGCAGAGGAAGCAGAAAATCATAGATTGTGGAACTCTCT
                                                                                        CTGTAATTCTGATGACCCCTACAACCCTTTAAATTTTAAGGCTCCTTTTCAAACATCAGG
                                                                                                                                            GGAAAATGAGAAAGGCTGTCGTGACTCAAAGACCCCATCTGAGTCCATTGTGGCCATTTC
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Rattus norvegicus (Norway rat)
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173899 GCTGCCGCTGTCAGAACAGCATCTGAACTTGTGGATTTCCGAGCGCTATCCCC 173840
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173279 TGGTTTTGATAGTGATGGCTCCCTGTCTGAATCAGACAGGGAACAGGGAACAAGACTCCGAAGGGCT
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                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
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184681: gap of unknown length
238285: contig of 53604 bp in length
239477: contig of unknown length
239477: gap of unknown length
240836: contig of 1259 bp in length
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llarity 72.3%; Pred. No. 1.9e-256;
Conservative 0; Mismatches 496;
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Web site: http://www.hgsc.bcm.tmc.edu/
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/organism="Rattus norvegicus"
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N Primer for synthesizing full-length cDNA and use thereof.
N BD148615.1
BUXATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BUXATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
BUXATYOTA; Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Islani,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primer for synthesizing full-length cDNA and use thereof
BD15.2
BD15.3
BD16.2002.9
BD16.2002.9
BD17.2002
BD17.3
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                                                                   172447 TTATAGACAACTGGCAGCTGTCCTTGGACATGGGTTTAAAGAAACGACTTGGTTCTA 172388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGATGTAGTTTAGTTATTTTTGGATAATGTGTCTCA-------TTAGAAACACAC 172339
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                                                                                                                                                                                                                            2426 AAACGAATTCAAGAAACAGAAGATGCTATTGGATATTGCTTGACATTTGAACACAGAAA 2485
                                                                                                                                                                                                                                                                                                                                                                                                         AGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTCTCAAGCAATGT 2545
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KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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                                            ACACATGTCAAAAGAAAAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCGCTGGGCAAGGCCGAGACTCTGTAGGCTTCCTCCGAATCCCGTCGACCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTCGGCGATCGCAAGCAGGCTCTTCTAAGTTCCCGACGCCTCTTGGCCCGGAAAACTC
                                                                                                                                                                                                                                                               ATTITIGGGTTCGGCTCCGCCCAGCCGGCCTACCCAGTCCTTCCGGTATCGCGTTG
                                                                                                                                                                                                                                                                                                      CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGGGGGCCGTGGGGGGGACT
                                                                                                                                                                                                                                                                                                                         AGGCGGATCGCGGAAACGGCTTGGCCCTCGGGCGGGCTTCCGGTTCTGGCCACCTTTTT
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                                                                                                                                                                                                                              1 ATTITIGGCTTCGCTTCCACCGCACCAGCCGGCCTACCCAGTCCTTCCGGTATCGCGTTG
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                                                                                                                                                                                         1,
/organism='Homo sapiens (human)'
Location/Qualifiers
                                                                                                                                                    Length 772;
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                                                                                                                                                  Score 738; DB 6; L
Pred. No. 4.2e-188;
0; Mismatches 8;
                                     1. .772
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/db_xref="taxon:9606"
                                                                                                                                                Best Local Similarity 98.8%;
Matches 752; Conservative 0
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AX868553 Sequence AC048369 Homo sapi G53188 SHGC-84724 AC112836 Rattus no	AX401620 Sequence AC127784 Rattus no	AC127924 RECURB IO BD020531 Novel gen BD100469 Novel gen BD15658 Primer fo	AA0.7350 acquence Continuation (2 of AC098930 Rattus no AC142019 Rattus no	AC135/40 Kattub no AC105660 RattuB no AC137459 RattuB no	AC139126 Rattus no AC139951 Rattus no	AC132069 Rattus no	AC121395 Rattus no AC121396 Rattus no AC128404 Rattus no	AC095816 Rattus no AC118529 Rattus no AC117053 Rattus no	AC096021 Rattus no AC110852 Rattus no	AC12912/ Maccus no AC127118 Mattus no AC126664 Mattus no	BC009873 Homo sapi Continuation (4 of	AC099380 Rattus no AC095250 Rattus no	AC124207 Rattus no AC121615 Rattus no AC129703 Rattus no	AC128070 Rattus no AC112286 Rattus no	AC128303 Rattus no AC128303 Rattus no AC096988 Rattus no	BD155096 Primer fo AX875034 Sequence	AX880750 Sequence AX023680 Homo sapi	AC097824 Rattus no	AC135370 Rattus no	AC127927 Rattus no AC129372 Rattus no	AC122442 Mus muscu	AC133242 Rattus no	AC098921 Ractus no AC132792 Rattus no	AY007107 Homo sapi	AC090439 Homo Bapi AC097188 Rattus no	AC111351 Rattus no AC122593 Rattus no	ACCESSOS ACTEUR NO	BX883047 Rattus no AC126912 Rattus no	AC140757 Rattue no AC110855 Rattue no	AC106182 Rattus no AC133127 Rattus no
772 166233 348 303230	540 6 268805 2	787 689 743 689 689 689 689 689	252921 2 89435 2	211582 2 240626 2 189173 2	231511 2 194401 2	258901 2	213967 2 227491 2	236858 2 324430 2 216261 2	234655 2 265515 2	174010 2 292004 2 231369 2	110000 2	244216 2 243534 2	256367 2 259169 2 304078 2	314884 2 272490 2	243044 2 286491 2	482 6	2148 6 2148 6 2148 9	238052 2	208175 2	250161 2	180516 10	197101 2	235178 2 245942 2	1366 9	220314 2	224803 2	297409 2	349571 10 171181 2	220229 2	235223 2
239.2 207.2 202.8 186.8	181.6	C 27 113.6 2 2 113.6 2 2 2 2 113.6 2 2 2 2 113.6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	31 108.4 32 105.8 33 103.8	103.8 103.8	37 103.6 38 103.4	103.4	42 102.2 43 102.2	102.2	47 101.4 48 101.4	49 101.2 50 101.2 51 100.8	100.6	54 100.2 55 100.2 56 99.6	9.66 66 66 66 66 66 66 66 66 66 66 66 66	60 99.6 61 99.4	63 98.8 64 98.4	8 8 6	0 80 80	97.8	97.6	74 97.6	97	76	79 97 80 97	81 96.6	96.6 96.6	84 96.6	9.96.98	96.6 96.4	90 96.4	92 96.4 96.4
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen	ic search, using sw model	September 15, 2005, 08:34:33 ; Search (without a 11635.782	1-650-482-3 3tcctccgtctcgcctg	IDENTITY NUC Gapop 10.0 , Gapext 1.0	4708233 seqs, 24227607955 residues	ts satisfying chosen parameters:	length: 0 length: 2000000000	Minimum Match 0% Maximum Match 100%	isting first	œ		gb_ov:* gb_pat:* gb_ph:*				umber of results predi or equal to the score	analysis of the total		duely Match Length DB ID	5.7 5367 10	6.7 215781 10	0.0 240836 2	0.9 200490 2 0.9 227054 2	0.9 248458 2	4.2 2942 6 4.2 2942 6	4.2 2942 9	4.2 5264 9 0.6 167079 9	0.6 328863 2 2.3 166233 2	9.0 257938 2	4.8 212115 2 AC116701 4.4 772 6 BD148615
J	nucleic	Sel	US-1(BCOre: 5468 :: 1 cgg	table: IDE Gag	47(number of hits	seq leng seq leng	Post-processing: Mi	3 ö	'' ·· ··	₩4.		0	400	14.	No. 18 greate	is defive	*	Score Mat	5234.2 95	, w <	* 4	m m	m (N N	CA C	N (N	0 4		262.6

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/ LTAIN 14 LOID *** METGTHRARKR PGPRIGSWFRLPFLRRSHACSSEFPPPSSRONP GNSALPERRTRYWTKLLSQLIALLPSLFQKLLLWSQLFGGI 1 PTRWLDFAASYSALRA GRSALPERRTRYWTKLLSQLLALLPSLFQKLLLWSQLFGGI 1 PTRWLDFAASYSALRA LDSAAPTFULEQQLWQCSSDLELPSSLGAGIVSRFRELDSSSGFELSGGIGGLYGRAY STLLP PSYLDYLPQUGGIRCQSSAGGGGIANGTHRELDSSSGFELSGGIGGIRCGSSAGGGGTWSFRUYSYLLN PSYLDYLPQUGGIRCQSSAGGGGYGFRTLFBSCYLESDGGHPQPLRAEMSATAWRRC PPLSTEGLPEIHHLRMKRLEFLQANKGGELPTPDQDNGYHSLEBEHNLLRMDPQHCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPAQAVSPAADRPEPTEKKPELVIQBVŠQSPQGSŠLFCELPVEKECEEDHTNATDLSD
RGESLPVSTRPVVATN"
                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 126 Row: n Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27597066. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 céccécceadadadegrerrererardardadecarereacaceceradadeceren 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Gaps
                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="MGC:66517 IMAGE:6830215"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.7%; Score 5234.2; DB 10; Length 5367; llarity 99.5%; Pred. No. 0; Conservative 0; Mismatches 18; Indels 10; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Ppp1r15b"
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Best Local Similarity
Matches 5345; Conserv
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                                                                                                                                                  FEATURES
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Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Vilalon, D.K., Mala, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Mizny, D.M., Sodergren, B.J., Lu, K., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Salska, U., Smallus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                       AC091537 Rattus no
AC145754 Rattus no
AC127136 Rattus no
AC096474 Rattus no
AC135741 Rattus no
AC110095 Rattus no
AC123154 Rattus no
                                                                                                                                                                                                                                                                                                                                                            Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 15b, mRNA (cDNA clone MGC:66517 IMAGE:6830215), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5367)
AC095802 Rattus no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                   ALIGNMENTS
                         AC145754
AC127136
                                                                                              AC096474
AC135741
AC110095
AC123154
     AC095802
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Strausberg, R.
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1.8 251382
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AUTHORS
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KEYWORDS
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1557 CTRETTCTA.COLACCAGCTCTATATATATATACAGCTCCCCCCCCCCCCCC
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CCCGCCGCCTTC 480 GTACTGGACCAA 637 GTACTGGACCAA 637 GTACTGGACCAA 637 GCTGCTTTGGAC 697 GCTGCTTTGGAC 697 GGTACTTGGACCAA 540 GAAGTTACAGCGC 757 AAGTTACAGCGC 757 AAGTTACAGCGC 660 GAAGTCTCTCAA 1116 TCAAGGCCCAGG 936 TTCAAGGCCAGG 936 TTCAAGGCCAGGA 1136 GAAGGACTCACATAG 1136 GAAGGATCATAGCC 1136 GAAGGATTCGTAA 1136 GAAGAATTGGTAA 1136 CAGAATTGGTAA 1136 CAGAATTGGTAA 1136 TACCCGTGGAAA 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: h Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORP
                                                                                               Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
                                                                                                                                                                     Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/#strain="FYDS/N"
/db xerf="FXDS/N"
/clone="IMAGE:3599662"
/tissue type="Mammary tumor. Metallothionien-TGF alpha model. IO month old virgin mouse. Taken by biopsy."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                 Sequencing Center Center Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCATGGGAAGAATTTGCAAGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAACAG
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                                                                                                                                              Gene Collection (MGC), Cancer Genomics Office, National Cancer
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                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: egapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                              (bases 1 to 3704)
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                                                                        Strausberg, R.
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Strauberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B. Buetow, K.H., Schaefer, C.R., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S.W., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hellen, B., Garcia, A.M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kazywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., and Marra, M.A.
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Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 115b, mRNA (cDNA clone IMAGE:3599662), partial cds.
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                                                                          GCCTGCAGACATGTCCTGATGGTGGCAAGAACAGAAGGATCTTTGACTGAAGGAGAAAAA 4972
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     1793 ACTGCAGCTTAACAACACTTGATTTCAGATGATTAGGTTTTTGTTTCTGAGACCCAGCAC 4852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTIGATAGCICAGATTATATTIGTATATTATTATTAACTAATCTGTAAATTGTAATAAA
                                                                                                                                                   GCCTGCAGACATGTCCTGATGGTGGCAAGAACAGAAGGATCTTTGACTGAAGGAGAAAAA
                                                                                                                                                                                                                                                     AGGCATGGTGGTTCTAGTTGAATACACATTCAAGTCTTGCAGTGGTGGTTTAGATCTGTG
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                                                      CTGTATATTTAAAAATTGTTCCAGATTACACCTTCACTATCAAATGAGTAAATGACTCAT
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1826 ATTOCHOACTTCAGTGGATTTTTTCCCCC-TTTTTTTTTTTTCCCCCAGAGCTGGAG	4370 AAGCAGAAAGGGCAGATAGAGCCAGAAAGTGCTAGTGTCCCCCCAAAGCGTGCTTC 4429 26.06 AAGCAGAAAGGGCAGATAGAGCCAGAAAGTGCTAGTGTCCCCCCCAAAGCGTGCTTC 2665 4430 TAGATAGTGTGTGAGTGGTCTTGTTTGTTCGTTAGCGTCACCTGTTGTGCATG 4489 26.66 TAGATAGTGTGTGACAGTGCTTGGTTTGTTCGTTAGCGTCACCTGTTGTGCATG 4789 26.67 TAGATAGTGTGTACCAGTTCTTTAGTGGTTACCAGTCACCTGTTGTGCATG 2725 4490 GTTGAGGTAATGTGTTACCAGTTCTTTAGTGGTTACATCACACAAAAGAGACCTCTGA 4549 2726 GTTGAGGTAATGTGTTACCAGTTCTTTAGTGGTTACATGCACACAAAAGAGACCTCTGA 4549 2726 GTTGAGGTGTGGTTACCAGTTCTTTAGTGGTTACATGCACAAAAGAGACCTCTGA 2785 4550 GTCGGGTGTGGGAATGACTTTCCAGACCTGGCAGGTAAACTTTATATAATCTC 4609 2786 GTCGGGTGTGGGAATGAGCTTTCCAGACCTGGCAGGAGACCTCTGA 2785 450 CTCGGTTATTCCGTTTACCAGACCTGGCAGGGTAAACTACCTCAGTTTATAAATCTC 2845 CTCGGTTATTCCGTTTAGTGGTCTAAAGTGCCTCAGTTTATAAATCTC 2845 CTCGGTTATTTCCGTTTAGTGGTCTAAAGTGCTCAGTGATGATGATCATCACCCCA 4729 4670 CACACAAGGTTAGTAAAGAGTCACCAGAAACGTGATGATGATCATCCA 2905
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2512 GGATCGAGTCAAAGGACTTACTGTTGTACAGCAATGTTAAGAAGTGAACCCTGCAACC 2571 2681 26	3292 TTGGATAACTATAAGCTCCATAGTCGTTCTAACTCAATTATGCATGGATTG 1526 TTGGATAACTATTAAGCTCCATAGTCAGTTCTAACTCAATTATGCATTGGTTG 1526 TTGGATAACTATTAAGCTTCAAATTAATGCGCTTTATGCATTTTTTTT

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Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Groepel, T., Campopiano, A., Chang, J., Chazaro, B., Choepel, T., Collangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dagar, K., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagot, J., Horton, L., Hulme, W., Illevil, Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., Marchan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Margan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Margan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Margan, F., Malor, J., Marquis, N., Matthews, C., McCarthy, M., Margan, F., Milor, R., Milor, R., Margan, C., Nochan, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Peters, N., Pollara, V., Raymond, C., Roteta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zohisision, M., Zumbek, L., Zimmer, A. and Zody, M., Wong, M., Zimmer, A. and Zody, M., Wong, M., Zimmer, A. and Zody, M., Wong, M., Wilson, M., Wyman, D., Ye, W.J., Young, G., M., Millon, M., Wyman, D., Ye, W.J., Young, G., M., Millon, M., Whyman, M., Ye, W.J., Young, G., Waller, M., Waller, M.
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Notice Submission

Notice Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

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(E. 4 (bases 1 to 215781)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Roguslawtkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, P., Corum, B., DaArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,

Rerreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kalls, C., Landersy, T., Levine, R.,

Indblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Maldrim, J., Meneus, L., Mihova, T., Olomaell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Setta, R., Rise, C., Rogov, P.,

Roman, J., Schubback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Talamas, J., Theodore, J., Theodore, J., Topham, K., Travers, M.,

Vassiliev, H., Venkataraman, V. S., Viell, R., Vo, A., Wilson, B., Wu, X.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submissed (122-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Oct 22, 2003 this sequence version replaced gi:37777388.
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Submitted (34-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Sa (bases 1 to 215781)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cook, P., Corum, B., Dartellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grander, P., Karatas, A., Kalls, C., Landers, T., Levine, B., Jones, C., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, B., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maddrim, J., Meneus, L., Micol, R., Norby, C., O'Donnoll, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, K., Valler, A. and Zody, M. Direct, Submission.
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                    TTTCTGTGTATTTTATGCACCTGCCTTTAGTGAACTCCAGAGTGCATTAAAGAGTCTGGT 4789
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                                                                                                                                                                                                                                                                                                                                                                           4790 TTAGTGCCGTGGGATGGGCTAGTTTAGAAGCTATGTTTGGAAAGCAGGCAAGTTGACTT 4849
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Mus musculus chromosome 1, clone RP23-30409, complete sequence.
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Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome I, clone RP23-30409
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 3 AC107842

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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         All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                           /clone="RP23-30409"
/clone lib="RPCI-23 Female Mouse BAC"
i. .8553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4828 . 4971
/ rpt family="BlF"
5328 . 5474
/ rpt family="Bl MM"
complement (6605 . 6614)
/ note="<30 qual SNGL region"
complement (668 . 664)
/ note="<30 qual SNGL region"
complement (6700 . 6708)
/ note="<30 qual SNGL region"
complement (6707 . 6743)
/ note="<30 qual SNGL region"
complement (6823 . 6844)
/ note="<30 qual SNGL region"
complement (6823 . 6844)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpc family="B3A"
complement (3608 . 3753)
/rpc family="B1 MM"
complement (3772 . 3900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="PBIDD10"
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/rpt_family="PBIDD9"
4828. .4971
                                                                                                                                                                      1. .215781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1304. .1512
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complement(1754. .1928)
/rpt_family="B3"
complement(2578. .2681)
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                                                                                                                                                                                                                                                                                                                                                                                                 complement (817. 1006)
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complement (1092. 1181)
/rpt_family="ID3"
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complement(2. .143)
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complement (3974, AAFA)
rpt family
                                                                                                                                                                                                                                                                                                                                            141. .478
rpt_family="(TTG)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  809. .2907
rpt_family="B1_MM"
902. .2957
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   complement (2. .143)
                                                                                                                                                                                                                                                                                                                                                                         76. - 815
rpt_family="(CA)n"
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156340 GACCATGGGAAGAATTTGCAAGGGATGGATGCAGGATACCAGAAACGAATTCAAGAAACAG 156399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156460 GGATCGAGTCAAAGGACTTACTGTTGTACAGCAATGTTAAGAAGTGAACAGCCTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2392 GACCATGGGAAGAATTTGCAAGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTIGCCATIGGCIACIGCTIGGCCTITIGAGCACAGAGAAAAATGTITAATAGACTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 215781;
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Pred. No. 0;
0; Mismatches 0;
                                                                                    /rpt_family="ORRID"
/rpt_family="ORRID"
/rpt_family="ORRIB=int"
/rpt_family="ORRIB=int"
9866_10062
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/rpt_family="ID_B1"
/rpt_family="ID_B1"
/rpt_family="ID_B1"
/rpt_family="ID_B1"
                                                                                                                                                                                                                                                                                                                                                                               complement (13030. .13132)
/rpt family="B1 kM"
complement (13345. .13408)
/rpt family="RSINE1"
complement (13429. .13690)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (15492. .15644) /rpt_family="B1_MM"
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8554. .8559
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|4513. .14624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="B4"
13830. .13980
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Best Local Similarity 99.9%;
Matches 3122; Conservative
                                                                     site: EcoRI
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                          159038
                                                                                                                                                                                                                                                            159098
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Rattus norvegicus clone CH230-146P11, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                   TIGITCCAGATTACACCTTCACTATCAAATGAGTAAATGACTCATGCCTGCAGACATGTC
                                                                                                   5031 CTGATGGTGGCAAGAACAGAAGGATCTTTGACTGAAGGAGAAAAACTGTCATTGTCATCC
                                                                                                                                                   158979 cricaricarcaacaacaacaacaacarcrirgacricaacaaaaaacricrcarricarcc
                                                                                                                                                                                                      5151 AGTTGAATACACATTCAAGTCTTGCAGTGGTGTTTAGATCTGTGTAGCATGTGAGGGCTC
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Rattus norvegicus (Norway rat)
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AC119774.6 GI:25095262
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4971
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Uniter Summission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23194778.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa. L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Man, J., Martin, K., Martinez, B., Mangua, P., Martin, K., Martinez, B., Minosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Norris, S., Martinez, B., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Ngupen, N., Norris, S., Pauk, K., Perez, L., Pfrankoch, C., Plopper, P., Poindexter, A., Peprov, Primus, E., Pu, L.-L., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, P., Poindexter, A., Pose, M., Rose, M., Reigh, R., Rives, C., Rodkey, T., Rohl, W., Rose, M., Rose, M., Rose, M., Rose, M., Savery, G., Scherr, S., Socht, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steimle, M., Strong, R., Suten, M., Thomas, M., Walle, M., Strong, R., Suten, M., Walle, M., Strong, R., Suten, M., Walle, M., Walle, M., Strong, R., Wu, J., Warren, R., Wen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Marren, S., Dunn, D., Von, N., Yu, F., Shan, M., Wan, M * NOTE: Bstimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). Worley, K.C.
Direct Submission
Submitted (102-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Center: Baylor College of Medicine Center code: BCM 3 (bases 1 to 212261)
Rat Genome Sequencing Consortium.
Direct Submission (bases 1 to 212261) Direct Submission Unpublished

us-10-650-482-3.rge

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-----AGGCAAGAGTTACCAACCCTGACCAAGACAATGGCTATCATAGCTTGGAGG
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                          AGTITIGIGGETITCCGAACACTAACCCCCAGAGACTGCTATCTTTCTGAAGATGGTTGTC
                                                                                                 AACTIGIGGATITICCGAGGGGTATCCCCAGAGAGCTGTTACCTTTCTGAAGGTGGTTGTC
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                             Length 212261;
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db xrefe"taxon:10116"
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142384 VETICAL/TOCAL/CATACITA/CHETA/ARAA/CATACITA/CAT	143420 TCAGTCTCCAGTACTGCAAGAAGAAAAACAGTCTTGGATAACTATAAGCTTCA 143476 3312 AGCCTCATAGTCAGTTCTAACTCAATTATGCATGCATTGAGTTCTTGTG 3361			4068 GGCTCTGTAGCTTTCAAGAATGGTAGAAATCATAAAGCACTCTTAAGTAATCATT 4125 144046 CTTTCGTAGCTCTCAAGAATGGCCAAAGATTGTAAAGCATTCTGGGAAGTGGTCATT 144102 4126 GCATTGTAGACTTTTTTTTTTTTTAACTAGGGGGTATTTGG 4166 144103 GCATTGTAGACTTTTTTTTTAACTTAGAGGCGTATTTGG 4166 144104 GCATTGTAGAATATTCACTTTTAACTAGAAGCTAAAACCAGGGGGTATTTGG 4166 144163 GCATTGTAGAATATTCACTTTTATTGTATTTTTTTTTTT
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                                                                                                                                                                                                                                                                                      Submitted (14-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On Nov 14, 2002 this sequence version replaced gi:22772949.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                           Direct Submission

Direct Submission

Submitted (17-SRP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (Dasea 1 to 240836)

Rat Genome Sequencing Consortium.

Direct Submission
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Welnstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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/clone="CH230-3B24" 1984. .3036 /note="wgs_contig"

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  DB 2;
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  Score 2188.8;
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Matches 3655; Conservative
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rtaaaataaccarccrccagaa 170167 | ||||||||||||| |BACAGTGGTGCTTTAGAGATCTG 169995 ACTGAAGGAGAAA-----A 5075 CCAAGGCAGGCAGGCAGGC 5135 IGCAGIGGIGCITI--AGAICIG 5193 CTTCTGAGGCTGAAATGTGGCA 5252 AATGACATTTTTGAGTTGGCCT 5342 recerecadacarer---- 5030 FIGATAGCICAGATTATATTTGT 5400 linear HTG 26-SBP-2002 Vertebrata; Euteleostomi; thi; Muridae; Murinae; CHED.

Aurany, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, Y., Aoyagi, A., Ayodeli, M., Baca, E., Baden, H., Baldwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, C., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, E., Charko, J., Chavez, D., Chen, E., Charko, J., Chavez, D., Chen, E., Char, Y., Chen, Z., Chard, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Dinh, H., Divya, K., Egar, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Dinh, H., Divya, K., Eraser, C., K., Edgen, C., Favan, C., Farser, M., Guevra, W., Garcia, A., Garrer, M., Guevra, W., Guraratne, P., Haaland, W., Handi, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A., Jackson, L., Jackson, L., Jackson, R., Johnson, B., Johnson, R., Johnson, R., Kovar, C., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C.,

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Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Louleaged, H., Lozado, K.J., Louleaged, H., Lozado, K.J., Mal. J., Mahabeshwari, M., Mahmadharin, M., Mahmadd, M., Martin, R., Malloy, K., Mangum, A., Mawhinez, E., Mangum, B., Maphuarin, M., Martin, R., Martin, R., Martinez, E., Mangum, B., Maphuaris, M., Martin, R., Martin, R., Martinez, E., Mangum, A., Manchi, M., Martin, R., Martinez, E., Milosavijevic, A., Milosavijevic, M., Morris, S., Monceanyor, J., Moore, S., Mankeris, C., Mania, E., Montemayor, J., Moore, S., Mankeris, C., Mania, E., Montemayor, J., Morris, S., Nasheris, C., Newloon, M., Nguyen, N., Norris, S., Nasheris, C., Newloon, G., Olarnpunsagoon, A., Pall, S., Parks, K., Papovic, D., Primus, E., Pull, S., Parks, K., Papovic, D., Primus, E., Pull, S., Parks, K., Pulazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M., Rei, Y., Reler, K., Regier, M., Ren, Y., Shorily, S., Reilly, M., Ren, Y., Router, M., Rese, K., Ruiz, S.J., Sonetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sheet, Y., Strong, R., Sutton, A., Svater, R., Tabor, P., Taylor, C., Taylor, T., Thomas, M., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valss, K., Wailson, M., Willson, R., Wailson, H., Walter, B., Wailson, R., Wailson, H., Walter, B., Wailson, J., Warten, J., Warten, J., Warten, J., Warten, J., Warten, J., Warten, J., Walten, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Walten, J., Walten, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Walten, J., Walten, J., Walten, J., Smith, D., Walten, J., Wal
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S Rat Genome Sequencing Consortium.
Direct Submission
L Submitted (16-5EP-2002) Human Genome Sequencing Center, Department Submitted (16-5EP-2002) Human Genetics Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ON Sep 26, 2002 this sequence version replaced gi:22771040.
The sequence in this sequence version replaced gi:22771040.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigned that consist entirely of whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GYZL
Center clone name: GYZL
Center clone name: GYZIO-194B23
Center clone name: GYZIO-194B23
Consensus quality: 131649 bases at least Q40
Consensus quality: 138620 bases at least Q30
Consensus quality: 138620 bases at least Q30
Consensus quality: 138620 bases at least Q20
Consensus quality: 138620 bases; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a "working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is sublitary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Worley, K.C.
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as soon as it is available and the accession number will be preserved.
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                                                   1 21048: contig of 21048 bp in length
149 108746: contig of 87598 bp in length
147 108846: gap of unknown length
1847 161819: contig of 87598 bp in length
1820 161919: gap of unknown length
1820 17640: contig of 52973 bp in length
1841 176740: gap of unknown length
176740: gap of unknown length
18747: contig of 10607 bp in length
18744: gap of unknown length
18744: contig of 10607 bp in length
1884 200499: contig of 13043 bp in length
Location/Qualifiers
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0; Mismatches 323; Indels
                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-194B23"
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89602. .91141
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. .188936
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19893. .21048
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21149. .23404
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29744. .33119
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18098. .50488
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71079. .72931
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[85991. .187347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="wgs_contig"
.3967. .15<u>9</u>51
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Anyal-bechi, V., Angaria, A., Angariano, D., Anyal-bechi, V., Angariano, D., Banachen, D., Banathen, B., Banathen, B., Banathen, B., Banathen, B., Banathen, D., Banathen, C., Corle, M., Calderon, E., Claver, D., Chaver, D., Deramo, C., Ding, Y., Dinh, H., Dayan-Rocha, S., Dhun, A., Dutbin, K., Daval, B., Eaves, Dearano, C., Ding, Y., Dinh, I., Daya, K., Deramo, C., Ding, Y., Dinh, H., Dayan-Rocha, S., Dhun, A., Dutbin, K., Daval, B., Eaves, D., Fernandez, S., Filhy, M., Falley, M., Farest, C., M., Gabisi, A., Gante, R., Garria, M., Gabrisi, A., Gante, R., Gardy, M., Garria, M., Gabrisi, A., Gante, R., Garria, M., Gabrisi, A., Gante, R., Garria, M., Gabrisi, A., Gante, R., Garria, M., Hanlen, S., Haldun, S.L., Manges, M., Harnandez, R., Haves, S., Huly, S., Hume, J., Jubay, H., Manger, M., Mallor, J., Luk, M., Liu, Y., Luh, W., Luh, W., Martin, R., Mangun, M., Martine, R., Mangun, M., Mangun, W., Mangun, M., Mangun, M., Mangun, W., Mangun, M., Mangun, W., Mangun, W., Mangun, W., Mangun, W., Mangun, W.,
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                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (07-NOV-2001) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153053 cecicerrecirrecrereracide contrace de contrace 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 214697 bases at least Q40
Consensus quality: 217252 bases at least Q30
Consensus quality: 219170 bases at least Q20
Estimated insert size: 224268; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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35184: gap of unknown length
224939: contig of 189755 bp in length
225039: gap of unknown length
227054: contig of 2015 bp in length.
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0; Mismatches 323;
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Center: Baylor College of Medicine
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/db_xref="taxon:10116"
/clone="CH230-191M14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas 3.0;
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                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Direct Submission
Submitted (10-JAN-2002) Human Genome Sequencing Center, Departmen
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                           AC105827.3 GI:23265261
HTG; HTGS_PHASE2; HTGS_DRAPT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Rat Genome Sequencing Consortium.
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                                                                                                                  Rattus norvegicus
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working differ" sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.ngsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                   Center project Information
Center project name: GNVL
Center clone name: GNVL
Center clone name: CH20-101J7
Assembly program: Phrap; version 0.990329
Consensus quality: 231489 bases at least Q40
Consensus quality: 232351 bases at least Q30
Consensus quality: 232350 bases at least Q30
Estimated insert size: 249328; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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0; Mismatches 323; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
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/note="clone_boundary
clone_end:Sp6
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/db_xref="taxon:10116"
/clone="CH230-101J7"
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                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
B 1 (bases 1 to 2942)
Cta T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
L. Patent: JP 2002191363-A 15534 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/15534
PD 09-JUL-2002
PP 28-JUL-2000
PP 200210-2001
PP 70SHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
             17-JAN-2003
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JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KBIICHI NAGAI, TETSUJI OTSUKI
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Location/Qualifiers
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    .2942
    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

             BD160691
Primer for synthesizing :
BD160691
                                                     BD160691.1 GI:27866449
JP 2002191363-A/15534.
Homo Bapiens (human)
Homo Bapiens
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72.5%;
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CTGATAATGAAGGATGAACTAGTGTGATTTCTAATCCTCCCTTTTTTGATTTAGTTGGAT 2790
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RDVISGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDA
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Catarrhini; Hominidae; Homo.
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Isogai, T. and Otenki, T.

Birect Submission

L. Submitted (10-MAY-2011) Takao Isogai, Helix Research Institute,
Direct Submission

Submitted (10-MAY-2011) Takao Isogai, Helix Research Institute,
Bubmitted (10-MAY-2011) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

Recommy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology; CDNA library construction,
5'- & 3'-end one pass sequencing and clone selection: Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
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NPLINFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVOLLGSQGSECPDSVO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 24.2%; Score 1320.8; DB 9; Length 2942; Best Local Similarity 72.5%; Pred. No. 0; Matches 1962; Conservative 0; Mismatches 662; Indels 84;
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/cell_type="teratocarcinoma"
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/db_xref="G1:14042485"
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/db_xref="taxon:9606"
/clone="NT2RP3002770"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (basea 1 to 5264)

Strausberg, K.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Banaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Malek, S.J., Bosk, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and mintial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: nisc mgg@nhgri.nin.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
                                                                                                                                                                                                                                                          2731 CTGATAATGAAGGATGAACTAGTGGATTTCTAATCCTCCCTTTTTTGATTGTTGGAT 2790
2611 ACAAATCTTGGCAGCTGTCCTTTGACATTTTTTTTTAGAGGAAATGTAACTTGGATCT 2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI 12-0CT-2004
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                                                                                                                                                  --- ACACCAACT
                                                                                                                                                                                                                       CCGATAATGAAGAAT -----CTCTTATCTGTAATCCTCTTTTTCCTATTTAGTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens cDNA clone MGC:74824 IMAGE:6172811, complete cds. BC065280 BC065280.1 GI:40807094 MGC.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                         CAGTITGATITITIGGGTAATGTGTCTCATTAGAA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Direct Submission
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AUTHORS
TITLE
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/ train lation="MEGTGGSRKRLGPRAGFRFWPPFPRRSQAGSSKFPTPLGPBN
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VSYLLNPSYLDCFPRLEQUMGYBLLPSSLOSRLYSRRELGSSPSGFLNIORIDNFSV
VSYLLNPSYLDCFPRLEQUSTGWSTGQTTTPESSCLREDHHPQPLSAELIP
ADWGGPPLSTEGLEBENSLLEBENGAGAGDLPTPOQNGYMSLEBENSLLRM
DFWRCNDPTQFPRAGDIPGNTGSTEEK ELLITTEVPLALEEESSPSGGCFSSEIPM
EKEPGEGRISVUDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDPEGEDWDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAARIVPEEPS
SEVDLSGSSDLENSQGSDLETPERSGEEDDWESSADEASSLKCLWNFRCNSDDPY
NPLNFKAPFQTSGERFGCEDSFTPSESIVAISECHTL.SGCKQLLSSQGSECPDSVQ
RDVLSGGRHTHVKRKKKCTPFLEEVTEYISGDEDRKGPWEEFARDGCRFQKRIQETEDA
                                                                                                             found
                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 140 Row: p Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 41282220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGTCGCCGCCGCGCGAGGGAGGGTCTTCTCTATGGTGGAGCGATCTCACACGGCCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 ACGTCTCCTTCCCTAGCCGGGATGGACCTAACCGCGGTCGCCACCGCTTGCGCGGGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 GAACCTCCTTCCC-CGCCAGGATGGAAGTCGCATCAGTCGCCGCCTATTGCGCGGGGTGT
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Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGYCLTFEHRERMFNRLQGTCFKGLNVLKQC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Young, A., Zhang, L.-H. and Green, E.D.
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/organism="Homo sapiens"
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Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping group, Further information can be found at
                                                                                                                                                                              ALG06489 167079 bp DNA linear PRI 08-NOV-2002 Human DNA sequence from clone RP11-739N20 on chromosome 1, complete sequence.
CTGATAATGAAGGATGAACTAGTGATTTCTAATCCTCCCTTTTTTGATTTAGTTGGAT 2764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr1
8h11-739N20 is from the library RPCI-11.3 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167079)
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests.clonerequestGanger.ac.uk On Nov 12, 2002 this sequence version replaced gi:22204251.
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Pred. No. 9e-273;
0; Mismatches 607; Indels 67; G
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Best Local Similarity 71.4%;
Matches 1686; Conservative
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AL627202 328863 bp DNA linear HTG 24-OCT-2002
Homo sapiens chromosome 1 clone RP11-174P23, 2 unordered pieces.
AL627202
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 328863)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 25, 2002 this sequence version replaced gi:20268846.
ATTGTCCAGGCTGTGGGTGAGGCTCTTGCTGGAGAAGATACACCCATATCAAGA
                                                           TCTCTGGCCATCATACCTTACTTTCTTGTAAGGCCCAGCTGTTAGAGAGCCAAGAAGATA
                                                                                            61577 Tricrigagrercacacerracrrecrrerraggreeagereragaagre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4, version 4.5 Sequencing vector: plasmid, L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: unlity: 17058 bases at least Q40 Consensus quality: 171825 bases at least Q40 Consensus quality: 172641 bases at least Q30 Insert size: 328763; amm-of-contigs Q20 Insert size: 17230; 12.6% error; agarose-fp Quality coverage: 2.67x in Q20 bases; sum-of-contigs Quality coverage: 5.15x in Q20 bases; agarose-fp
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6944 7043: gap of 100 bp
7044 328863: contig of 321820 bp in length.
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Center: Wellcome Trust Sanger Institute
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Web site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
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/clone="RP11-174P23"
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1. .6943
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HTG; HTGS PHASE1; HTGS CANCELLED.
Homo sapiens (human)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldakin, J., Barra, N., Bastreho, V., Beda, F., Boyalavki, J., Barra, N., Bastreho, V., Bada, F., Boyalavki, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Kardyna, S., Ginde, S., Goyette, M., Graham, L., Kardyna, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Katin, J., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, J., Maranda, C., Mlenga, V., Morrow, J., McCarthy, M., McEwan, P., McGurk, T., Mardand, C., Mlenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Plerre, R., Kothman, D., Stange, Thomann, N., Stopanod, C., Riley, R., Spencer, B., Santos, R., Schauer, S., Severy, P., Spencer, B., Tragillo, J., Vonna, N., Stopanod, C., Riley, R., Waman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Travers, M., Tr
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                                                                                                                                                                                                                                                                            CAGGGAAGAATTGGAAAGGCCGTCAGGACTCAAAGGCCTCTTCTGAGGTCACAGGGCCT 2205
                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCTGGCCATCATACCTTTCTTGTAAGGCCCAGCTGTTAGAGAGCCAAGAAGATA 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGTCCAGGCTGTGGGTGAGGCTCTTGCTGGAGAAAGATACACCCATATCAAGA 2325
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166233)
                                                                                                                     CTTTCTGTCATTCTGAGGACCCCTACAACCTTTTAAATTTTAAGGCTCCTTTTCAACCGT
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Web site: http://www-seq.wi.mit.edu
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AC048369.2 GI:8705131
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOWD 88piens (human)
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NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                  Center Clohe name: 284_G5
Sequencing vector: M13, M77815, 100$ of reads
Sequencing vector: M13, M77815, 100$ of reads
Chemistry: Dye-terminator B1g Dye; 100$ of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 151910 bases at least Q30
Consensus quality: 158917 bases at least Q30
Consensus quality: 161704 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 163433; aum-of-contigs
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
Center_project_name: L8045
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contig of 6210 bp in length
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contig of 6888 bp in length
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contig of 8060 bp in length
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contig of 8951 bp in length
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bp in length

contig of 7798

us-10-650-482-3.rge

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110 120552: contig of 11443 bp in length 1553 120652: gap of 100 bp 1553 130699: contig of 10047 bp in length 130799: gap of 100 bp 15070 130799: gap of 100 bp 15070 145936: contig of 15137 bp in length 1593 166233: contig of 20197 bp in length 1507 166233: contig of 20197 bp in length 1. 166233
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1. .1069
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note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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GenCore version 5. Copyright (c) 1993 - 2005 C	OM nucleic - nucleic search, using sw model	Run on: September 15, 2005, 08:08:59; (wit	Title: US-10-650-482-3 Perfect score: 5468 Sequence: 1 cggtcctccgtctcgcctg	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 4390206 seqs, 2959870667 residues	Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100%	first	z'		: geneseqn2001bs : geneseqn2002as : geneseqn2002bs	8: genesegn2003as:* 9: genesegn2003bs:* 10: genesegn2003cs:*	11: genesequ2004as:* 12: genesequ2004as:* 13: genesequ2004bs:*	1. No. is the number of results pr re greater than or equal to the sc	al		Rebuic No. Score Match Length DB ID	5468 100.0 5468 12 1324 24.2 2942 12	1320.8 24.2 2942 4	542.6 9.9 883 4	181.6 3.3 540 6 ABK63389	9 170.8 3.1 399 8	11 109 2.0 421 9	12 109 2.0 543 4 13 99.6 1.8 1028 3	98 1.8	98 1.8 2148 b 98 1.8 2148 10	218 3 100610 12 1678 2

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Matches 5468; Conservative
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Acn45088 Mouse gen
Adg97855 Mouse can
Aba77056 Prolitera
Adi35834 Rat proop
Acn44124 Mouse gen
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4462. 2558
/*tag= a //trag= //product= "Mouse GADD34-like (GADD34L)
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 ADP72921
AAZ61522
ACN45088
ADQ97855
ABA77056
ADI35834
ACN44124
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P-PSDB; ADQ88460.
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	1261 CAGAGATGTCGGCAACCGCCTGGAGAAGGTGTCCGCCTCTCTCT	GCCGGAGCCCTGAGAAAAACCAAATTGGTGATTCAGAGAGTTTCACAGAGCCCCC GCGGAGCCCACTGAGAAAAACCAGAATTGGTGATTCAGAGAGTTTCACAGAGCCCCC GCGGAAGCAGTCTGTTTTTTTTTGGAATTACCCGTGGAAAAAAAA	1681 GCAACAAACTGATAGATTATTTGGGAGGCCCCCCAGTGACTTGGAAGCCTCTG 1740 1741 ATTCTGAAACTGATGATTATTTTGGGAGCCCCCCAGTGACTTGATGATGCCTCTG 1740 1741 ATTCTGAAAGTGAGGATTGGGAACCTGAGGACGATGGCTTTGATAGCGATGGCT 1800 1741 ATTCTGAAAGTGAGGATTGGGAACCTGAGGACGATGGCTTTGATAGCGATGGCT 1800 1801 CCCTGTCTGAATCAGAGCTTGGAACAGGACTCCGAAGGCCTTTCGAAGCCTTTCC 1860 1801 CCCTGTCTGAATCAGACGTGGAACAGGACTCCGAAGGCCTTCACCTTTCC 1860 1861 ACAGTGTAGAATCAGAACACTTTACAGCCCACCAGAA 1920 1961 ACAGTGTAGAACCCTTACAAACTTTACAGCCACCAGGATTCAGACGCTGCCAGAA 1920 1921 TTGCCCCCAGAAACCTTTACAGCCACACCTTGGCAGCTGCAGGAA 1980 1921 TTGCCCCCAGAGACCCATCAGAACTTTACAGCCACACTTGGCAGCTGTAGGAA 1980 1921 TTGCCCCCAGAGACCCATCAGAACTTTACAGCACCCTTCGGCAGCTGTAGGAA 1980 1981 1161

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Pred. No. 0;
0; Mismatches 660; Indels
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407. .2548
/ttag= a "Human GADD34-like (GADD34L)
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                                                                                                                                                                                    CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.5%;
Matches 1964; Conservative
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P-PSDB; ADQ88458.
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TGGCAGCCTGTAGTCCTAGCTAGCATACACTACCTCTTACCTGAGAGGTGTCTTTTAAAA
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                                                   GTTTAATAGACT ----GAGGATCGAGTCAAAGGACTTACTGTTGTACAGCAATGTTAAGA
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                                                                                        TGAGGATCGCAAAGGACCATGGGAAGAATTTGCAAGGGATGCAGGTTCCAGAAACG
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A, Nagai K,
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T, Wakamatsu
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                                                                  TCCGGCCTCGTGGCAGGGATGTCCACCTCTTTCTACGGAAGGCCTACCAGAAATTCACCA
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                                                                                                       CCTTCGTATGAAACGGCTAGAATTCCT---CCAGGCTAACAAAGGGCAAGAGTTACCCAC
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particularly the 5602 full-Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

ID NO 18964; 2537pp + Sequence Listing; English. 8; SEQ Claim

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotide which comprises a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 3'-end a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
coligonucleotide comprises a 1'-end sequence, where the
coligonucleotide comprises a 1'-end sequence, where the
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coligonucleotide which comprises a 1'-end sequence, where
coligonucleotide comprises a 1'-end sequence, where
coligonucleotide which comprises a 1'-end sequence, where
coligonucleotide which are sets can be used in antisens encoded by
the full-length cDNAs. The primers are also useful for the
coligonucleotides, all of which are used in the exemplification of the present invention

Sequence 2942 BP; 731 A; 741 C; 726 G; 744 T; 0 U; 0 Other;

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270 330 509 454 266 514 611 671 634 crcaaagarceeccresaecaecaececcaceecreeecaaeeccaaecceaeacrererageer 334 672 CTATTCCAGAAGCTGCTGCTTTGGAGCCAGCTTTCCGGGGGCCTGATTCCTACCAGATGG 731 211 ACGTCTCCTTCCCTAGCCGGGATGGACCTAACCGCGGTCGCCACCGCTTGCGCGGGGCCTC GGCTTCCGGTTCTGGCCACCTTTTTCCCTCGGCGATCGCAAGCAGCACCTTCTAAGTTC ------GCTCTGCCC CCGTCGCCGCCGCGCGAGGGAGGGTCTTCTCTATGGTGGAGCGATCTCACACGGCCTAGG ccarceceasecereseseacrecrarecaresterreasecereaseceasecare GAACCTCCTTCCC-CGCCAGGATGGAAGTCGCATCAGTCGCCCCCTATTGCGCGGCTGT TGGCCGTCCGGTGCAGCACTCGTTGCGGAAGCCGCCGCTCTCTGGGCCTCTCTGCCGG TCTTCCCTGTGTTCTGCCGCCCGCTGCCGCATTCGCTGCCCTCTGTGGCTTTTCTGCTGG CGCGGGAATCGGACTGCAGTACCCACTCCGTGGCTGGGCAAGGCGGAGACTGTGTAGACC TCGGATCCAGCCTGCGCTGACGCCGCTGAGCTCTGTCCTCCTCCTGTCTGAGAAGCCGCC AAG-GAAAGGAGATGGAGACAGGAACGCACAGGGCCCCGGAAGCGGCCTGGCCCTCGGCTG <u> naganana de de deserces de deserces de de anordes de contra de c</u> GGCTCCTGGTTCCGGCTGCCC - - TTCCTTCGGCGATCGCACGCCTGCTCTTCGGAGTTC cciandecretresecessana en cessan en conservates en contra GAGCGTCGGACCAGGTACTGGACCAAATTGCTTTCTCAGCTCCTTGCCCTGCTCCCTAGC GAGACTCGGGTCAGTTACTGGACGAAACTGCTCCCCAGCTCCTTGCGCCGCTCCCCGGA Gaps Length 2942; 84; 662; Indels DB 4; CCGCCGCCTTCCTCGACAAATCCCGGGAACTCC-24.2%; Score 1320.8; 72.5%; Pred. No. 0; ive 0; Mismatches Query Match Best Local Similarity 72.5 Matches 1962; Conservative 151 395 210 515 96 156 271 215 275 335 451 455 567 612 575 331 391

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1290 1350 1387 1447 1410 1600 1660 1650 1710 1030 1090 1150 1210 1551 AGAGAGCTGCTATCTTGAAGATGGTTGTCACCCTCAGCCGTTGCGGGCAGAGATGTC 1270 1531 TTTGGAAGAAGAGAGCCCTTCTGAGGGCTGTCCATCTAGTGAGATACCTATGGAAAAGGA 1590 TGACTTGGAAGCCAGCTCTGATTCTGAAAGTGAGGATTGGGGGGGAAGCCTGAGGACGA 1780 810 694 791 754 851 911 870 970 criadadecadecididadadadadadecidiridececadidadeciricaarecedicidaa 990 TGCTTCAGAAGGTGCTAATTTGGAGCCAACTTTTCGGTGGAATGTTTCCGACCAGATGG AGTCAGCTATCAGAACAGTGATGGAAATAGCGAGGTAGTCGGCTTCCAGACACTAACCCC 1411 TCCAAAACACTGCAGAGATAACCCAACACATTGTTCCTGCTGCTGGAGACATTCCTGG TTCTGCCAGACCAGCTTGTAGTAACAACTGATAGATTATATATTTTGGGAGGTGCATCCAG CTAGATTTTGCCGCAAGTTACAGCGCCCTGAGAGCTTCGAGAGGACGGGAATCTGAC GCTCCCACGGTGCAGAAGTCTCTGAGTTACACTGCGGCTGGACTCTTCGCGAAGACTCGC GCCCCCACAGCGCAGAATCTTTGAGTT-CGCTGCAGCTCGACTCCTC---AGACCCCTC GTCGTCAGTACTCTTGCATTGGCTAGAGGAGGACTCCAGTGGCAGTGCTCGTCCTCAGA gercaccagrecerrearregeragaggaaggarecacregeaaraeregeeeegaa - CTGGAAGTTAAACTCAAGGCCCAGGAAAGAGCTTTAGACTCTGCAGCGCCCACTTTCCT 871 CCTAAAATTGGAGCTTAAGGCCAAGGGAAGTGCTTTGGACCCTGCAGGCACAGGCTTTTCT CCTGGAGCAGCTGTGGGGAGTGGAGTTGCTGCCCAGTAGCCTTCAAGCTGGTCTAGT CTCCCACCGAGAACTTGACTCTTCATCCTCTGGGCCTCTGAGGCTTCAGAGCTTAGGTAA CTCTAACCGGGAACTTGGCTCTTCGCCCTCTGGGCCTCTAAACATTCAACGCATAGACGA TTTCAAGGTAGTTTCCTATCTCTGAACCCTTCCTACCTGGACTACCTTCCCCAGTTAGG GCTGCGCTGTCAGAGCAGCGCTGGAGGTGGCCAGTTTGTGGGTTTCCGAACACTAACCCC Acadacaccrecercadadacaccarrerearececadececercadececadaacecar GGCAACCGCCTGGAGAAGGTGCCGCCTCTCTACAGAAGGCCTGCCGGAAATCCACCA rcceectrcereecaggarerccactrcrrcracegaaggccraccagaarrcacca CCTTCGTATGAAACGGCTAGAATTCCT---CCAGGCTAACAAAGGGCAAAGAGTTACCCAC CCCTGACCAAGATAATGGCTATCATAGCCTGGAGGAGGAACATAACCTTCTCCGGATGGA cecreaceacearanarescraceacacecresassassascasecrreressares CCCACACAACATTGCACAGATAACCCAGCACAGGCGGTGTCCCCTGCTGCAGACAGGCC--------GGAGCCCACTGAGAAAAACCAGAATTGGTGATTCAAGAAGTTTCAC---1471 AAACACCCAGGAATCCACTGAAGAAAAATAGAATTATTAACTACAGAGGTTCCACTTGC gccricaadadesccaaraacreracricarracrearacradaadereacerrecer TTCTACCAGACCAGTTTGTAGCAACAAACTGATAGATTATATTTTGGGAGGCGCCCCCAG ------AGAGCCCCCAGGGAAGCAGTCTGTTTTGTGAATTACCCGTGGAAAAAAA 732 792 755 852 1031 1091 1051 1151 1111 1111 1271 1231 1331 1388 1351 1448 1505 1552 1591 1991 1651 1721 695 811 912 971 931 991 1211 8 엄 ò 셤 ሯ 셤 ઠ 용 ò 용 à 용 ઠે 요 à 셤 ò g ò 셤 ò 원 ઠે g 8 셤 ò g Š 유 8 g ò 셤 à

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
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                                                                                                                                                                                                                                                                                                                Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective, vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; neural disorder; muncal esystem disorder; muscular disorder; wound; reproductive disorder; gastrointestinal disorder; infectious disorder; cardiovascular disorder; renal disorder; infectious disorder; cardiovascular disorder; renal disorder; infectious disease; cardiovascular disorder; se.
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                                                                                                                                                                                                                                                     cancer antigen nucleotide sequence SEQ ID NO:168.
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624 AGGTACTGGACCAAATTGCTTTCTCAGCTCCTTGCCCTGCTCCCTAGCCTATTCCAGAAG 683		283 GGAGICIACAGCCCCTGAGAGCCCTGAAGGACGGGAGAAACCAGCCGCCCCCACAGCG 342 904 CAGAAGTCTCTGAGITACACTGCGGCTGGACTCTTCGCGAAGACTCGCGTCGTCGTCAGTACT 863 913 CAGAAATCTTTGAGIT-CGCTGCAGCTCGTCAGACCCCTCGGTCACCAGTCC 398 914 CAMACCAMACCAMAGAACAACAACAACAACACAAAATCTTCAAAATCTTTGAGAAATCTTTGAGAAATCTTTGAGAATCAAAAATCTAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAATCAAAAAA		GCTGTGGGGAGTGGAGTTGCTGCCGCAGTTCAGTGGTTGTTTTTTTT		639 ATCCTATTIGCTGAACCCTTCCTACCTGGACTGCTTTCCTAGGAAGTCAGCTATCA 698 1163 GAGCAGCGCTGGAGGCGAGGTTTGTGGGTTTCCGAAACCCCCAGAGGCTGCTA 1222 1164 GAGCAGCGCTGGAGGTGGCGTTTGTGGGTTTCCGAAACTTAGTGCTAGTAGTGAGGGTGCTA 1222 1165 GAGCAGGAGAGAAAAACGAGGAGAAAAAACGAGAGAGAG	TCTTTCTGAAGATGGTTGTCACCCTCAGCCGTTGCGGCAGAGATGTCGGCAACCGCCTG 1282	GAGAAGGTGTCCGCCTCTTACAGAAGGCCTGCCGGAAATCCACCACCATCGTATGAA	1343 ACGGCTAGAATTCCTCCAGGCTAACAAAGGTTACCCACCCCTGACAAA 1399	CACAGATAACCCAGCACAGGGGGGTGTCCCCTGCTGCTGCGCC	1508 GCCCACTGAGAAAAAACCAGAATTGGTGATTCAAGAAGTTTCACA 1552	CCCACTARIGGAACTGACCTCTGAGTAGAGAGAGAGGCTTCCTGTTTCTACCAGACC 1672 CCGAATAAGTGTAGTTGATTACTCATACCTAGAAGGTGACCTTCCCCATTTCTGCCAGACC 1238 AGTTTGTAGCAACAACTGATAGATTATTTTGGGAGGCGCCCCCAGTGACTTGGAAGC 1732

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AAM25965. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiavascular; antianaemic; antiantearia; antianaemic; antialactic; valuerary; cardiavascular; antianaemic; antialactic; valuerary; antialactic; osteopathic; dermatological; antialactic; valuerary; antialactic; cytostatic; neuroprotective; antidaperic; cytostatic; neuroprotective; antidaperic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidapersesant; nootropic; antidabetic; cytostatic; neuroprotective; antidapersesant; nootropic; conding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polymucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cereoproresis, severe combined immunodediciency, eczen, alleiner; allease, cancer, multiple solerosis, depression, allease, parkinson's disease, neurodegenerative and
                                                                                                                                                                                     antilificammetory; antilificanticitic; immunosuppressive; antilificammetory; antilificanticitic; immunosuppressive; antilificammetory; antilificam
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                                                                                                                                                                cancer; ulcer; HIV infection; human immunodeficiency virus;
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                                                                                              Human protein encoding cDNA sequence SEQ ID NO:224.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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                               (first entry)
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P-PSDB; AAM25448.
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                                                                                                                  CTTCACCTTTGGAACTCTTTCCACAGTGTAGATCCTTACAAACCCCAAAACTTTACAGCC 1898
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1719 AGTGACTTGGAAGCCAGCTCTGATTCTGAAAGTGAGGATTGGGGCCGAGGAACCTGAGGAC 1778
                                                          GATGGCTTTGATAGCGATGGCTCCCTGTCTGAATCAGACGTGGAACAGGACTCGGAAGGC 1838
                                                                                                                                                                              1899 ACGATTCAGACGGCTGCCAGAATTGCCCCCAGAGACCCATCAGATTCAGGGACATCCTGG 1958
                                                                          181 ACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCTTCTGATTCAGAGAAGGATTTG 240
                                                                                                                                                                                                                                                                                                                  CATAGTICTGGGGAGGAAGATGACTGGGAATCTAGTGCAGATGAAGCAGAGAGTCTTCAA 360
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                                                                                                                                               121 CTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAGCA 180
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                                                                                                                                                                                                                                         TCTGGCAGCTGTGGTGTAGGGA---GCTGTCAGGAGGGACCCCTTCCGGAGACCCCCGAC
                    1 AGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGATTGGGATGAGGAAGCTGAGGAT
                                                                                                                                                                                                                                                                                                 CATAGTTCCGGGGAGGAAGATGACTGGGAACCGAGTGCAGATGAAGCAGAGAATCTTAAA
                                                                                                                                                                                                                                                                                                                                                                         361 ACTGTGGGAACTTCATTCTGTTAATTCTGGATGGACCCCTACAACCCTTTAAATTTTAAG
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Score 542.6; DB 4; Length 8 Pred. No. 5.8e-129; 0; Mismatches 154; Indels

Query Match 9.9%; Best Local Similarity 80.5%; Matches 688; Conservative

454

394

999 514 611 574 671

731 694 790

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Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAGATTTTGCTGGAGTCTACAAGCGCCCTGAAAGGACCAGAAAGCAAG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence differentially expressed in response to a hepatotoxin #1296.
                                                                                                                                                                                           AAGAAAAAGGAGATGGAGCCGGGGACAGGCGGATCGCGGAAACGGCTTGGCCCTCGGGCCG
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   TCCTCCGAATCCCGTCGACCTCCAGCCGCTGAGCGCCGCGCCCCTACCTGAGAGACTGTC
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differential expression; centrilobular necrosis; steatosis.
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11-MAY-2001;
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length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotides, or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
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complementary strand of the primers are also useful for the complementary complementary strands and complementary strands and complementary compleme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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, Sugiyama T, Wakamatsu A, Nagai K,
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-001877677
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                                   The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in unexposed to the capbounds or progression of these toxic effect, preferably the compound or progression of a toxic effect, preferably the cap cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the expression in a tissue or cell sample exposed to the compound of two or cap genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression of the genes is indicative of at least one toxic effect or progression. The methods utilise a set of at least two probes (on a solid to support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell sample to present information confidentially markers in drug screening and toxicity markers in drug screening and toxicity markers in drug screening and toxicity sasays. The genes and the prediction or identification of identifying toxicity markers in drug screening and toxicity sasays. The present compound or agent the present compound or agent the present compound or agent the sample that has been expressed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present compound or agent to a hepatotoxic agent and a differentially expressed in response to a hepatotoxic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TCATGCCTGCAGACATGTCCTGATGGTGGCAAGAACAGAAGGATCT----TTG
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llarity 75.8%; Pred. No. 6.8e-36;
Conservative 0; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 540 BP; 162 A; 119 C; 85 G; 174 T; 0 U; 0 Other;
    Claim 1; SEQ ID NO 1296; 239pp; English.
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Matches 388; Conserv
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The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile cof a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity markers in sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TCATGCCTGCAGACATGTCCTGATGGTGGCAAGAACAGAAGGATCT----TTG 5060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4960 ATATTTAAAAATTGTTCCAGATTACACCTTCACTATCAAATGAGTAAATGAC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .8e-36;
es 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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llarity 75.8%; Pred. No. 6.8e
Conservative 0; Mismatches
5398 TGTATATAATTAACTAATCTGTAAATTGT
                                  claim 1; SEQ ID NO 2776; 1156pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                              Toxicity-related gene, SEQ ID 2776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug screening; toxicity assay; ds.
                                                                                                                                                                                                                                  BP.
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15-MAR-2002; 2002US-0364045P.
15-MAR-2002; 2002US-0364055P.
30-DEC-2002; 2002US-0436643P.
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ID ADB57750 standard; DNA; 540
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212
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                                                                                                                                                                                                                                                                                                        The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine, 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                            5121 GGCAGGCAGGCAGGCATGGTGGTTCTAGTTGAATACACATTC-AAGTCTTGCAGTG
                                                        ACTGAAGGAGAAAACTGTCATTGTCATCCCAGCCCCCAGGAAAGAACACCTCCAAGGCA
                                                                                                                                                          ------AGGCAGGCATGGCGGTTCTAGCTGAACACTTACACTCAGTCTTGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTATATATTATTAACTAATCTGTAAATTGT 5429
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MATHIALAGAN N.
TAO N.
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15-DEC-1999;
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cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 muclecide sequences, appearing as ABX50072-ABX55933, or complements of them. Also included are popearing as ABX50072-ABX55933, or complements of them. Also included are if it a transformed cell having a nucleic acid comprising an LMFD nucleic acid dinked to a promoter and a 3, non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and comprising a level or pattern of a molecule in a bovine cell or tissue comprising a level or pattern of a molecule acid (comprising any of the 5912 nucleic acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the detecting a level or pattern of the molecule; The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for geneme mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the 5912 to prededing, preparation of constructs for use in cattle gene expression, or the molecule. The present sequence is one of the 5912 complementer forms the specification but was obtained in sequence. Sequence was not shown in the specification but was obtained in sequence according the level or better forms the usproved of the present sequence. The present sequence was not shown in the specification but was obtained in sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2503 ATAGACTGAGGATCGAGTCAAAGGACTTACTGTTACAGCAATGTTAAGA--AGTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 CTTCAAGCAAACATGTTTCAAAGGACTTAATGTTTTCGAGCAATGTTAAGATGATTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2330 AAAGGTAACCTTCCTGGAAGAAGTTACTGAGTATTATATAAGTGGTGATGAGGATCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 ATAGGTAACCTTCCTTGAAGATTACTGAGTATTACATAAGCGGTGATGAGGATCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2450 AGAAGTTGCCATTGGCTACTGCTTGGCCTTTGAGCACAGAGAAAAA----ATGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2561 AGCCTGCAACCCGTGCCCACTCTGTCTTTACTTGAGAGTTTCCCTTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neuroblastoma expressed polynucleotide SEQ ID NO 2769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 399 BP; 133 A; 62 C; 82 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 170.8; DB 8; llarity 79.1%; Pred. No. 3.5e-33; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2001; 2001WO-JP001629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2001 (first entry)
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es 231; Conserv.
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             LABAT I.
STACHE-CRAIN B.
DICKSON M C.
                                                                                      Drmanac RT, Labat I,
                                                                                                                                                                                           antisense DNA or RNA
DRMANAC R T.
                                                                                                                   WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 187; Conserv
                                                        JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH11666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
             (LABA/)
(STAC/)
(DICK/)
 (DRMA/)
                                                        (JONE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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 MX BX BX BX BX B
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                                                                                                                                                                                                                                 The invention relates to novel genes (AAI99926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in disgnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGACTCTAAATTGGCTTCTACAGATCAATAATTTAAATGTAACTAGTTGGGATTTTATAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, 88; sequencing by hybridisation; SBH; expressed sequence tag; BST;
genome mapping; biodiversity; genetic disorder.
                                                                                                                                 Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumor marker for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5272 ATCAAAACCGTCAAATTTTTTTTTT-----TATAATTTAAGAAAGAGTTGGGGAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5214 ACAGGTGGGGCCACACTTCTGAGGGCTGAAATGTGGCAACCCTTTATC--TAACTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 ACAGGTAAAAGTTCCATTTCTGAGTGATGAAATGTAACGTTCTTCATCTTTAACTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5326 ATTTTTGAGTTGGCCTTTTCAGCTCAGTTT-TACGTGTAACGTGGAGATTTGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 113.6; DB 4; Length 689; Best Local Similarity 72.3%; Pred. No. 2.8e-18; Matches 191; Conservative 0; Mismatches 64; Indels 9;
                                                                                                                                                                                                                                                                                                                                          Sequence 689 BP; 221 A; 114 C; 93 G; 251 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5468
                                                                                                                                                                                                       Claim 1; Page 2028; 2979pp; Japanese.
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                           CHIBA PREFECTURE.
HISAMITSU PHARM CO LTD.
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07-MAR-2000; 2000JP-00159195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human leukocyte cDNA #745.
                                                                                                     WPI; 2001-565584/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003073623-A1
                                                                         Nakagawara A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACH49151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                           ( WSIH)
                             (CHIB-)
                                                                                                                                                                               agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisenses DNA or RNA. The purified polypeptide is useful for generating antisense specific for it. The present sequence is useful as a double form part of the printed specification, but was for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCAAAACCGTCAAATTTTTTTTTTT----TATAATTTAAGAAAGAGTTGGGGAATGAC 5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6 ATTTTTGAGTTGGCCCTTTTCAGCTCAGTCATTT-TACGTGTAACGTGGAGATTTGATAG 5384
                                                                                                                                                                                 New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 ACAGGTAAAAGTTCCATTTCTGAGTGATGTAACACTTCTTCATCTTAACTTGAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ATCAAAACTATCAGATTTTATTTTTTTAAAGGAAGGTAAAGTTAGGGGACTAGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AGACTCTAAATTGGCTTCTACAGATCAATAATTTAAATGTAACTAGTTGGGATTTTATAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5214 ACAGGTGGGGCCACACTTCTGAGGGCTGAAATGTGGCCAACCCTTTATC - TAACTTGAA
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         Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 421 BP; 158 A; 50 C; 69 G; 144 T; 0 U; 0 Other;
Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%; Score 109; DB 9;
llarity 71.6%; Pred. No. 3.2e-17;
Conservative 0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA clone (3'-primer) SEQ ID NO:8501.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 36363; 44pp; English.
    Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5445 AATTATTAAAAAAAAAAA 5465
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Or an oligonucleotide comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, 1'-end sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH13633 to AAH18742 represent human cDNA sequences, AAB92446 to AAB95893 represent human amino acid sequences, and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 8501; 2537pp + Sequence Listing; English
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Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                          27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-002418997.
                                                                                                                                                                                                      28-JUL-2000; 2000EP-00116126
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                               Homo sapiens
                                                                                   BP1074617-A2
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ŝ 2407 TTGCAAGGGATGCAGGTTCCAGAAACGAATTCAAGAAACAGAAGTTGCCATTGGCT 2466 2467 ACTGCTTGGCCTTTGAGCACAGAGAAAAATGTTTAATAGACT----GAGGATCGAGTCA 2522 CTGTCTCTTACTTGAGA-GTTTCCCTTAAAAACAAACACTGGCAGCTGTCCTTGGACATG 2640 AAGGACTTACTGTTGTACAGCAATGTTAAGAAGTGA-ACAGCCTGCAACCCGTGCCCACT 2581 543 TTTNCAAGGATGAATCCAGTTCCNAGAANGGATTCCANGAACCAGAAGATGCTATTGGAT 484 483 ATGGCTTGACATTTGACCCCAGAGAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCA 424 363 CTACCTCTTACCTGAGAGGTGTCTTTTAAAAACAAATCTTGGCAGCTGTCCTTTGACATT 304 26; Gaps Query Match 2.0%; Score 109; DB 4; Length 543; Best Local Similarity 63.7%; Pred. No. 3.8e-17; Matches 254; Conservative 0; Mismatches 119; Indels : 2523 2582

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2701 CATTAGAA-----CTCTTATC 2740 243 CACTCAGAAACATTCAGGTTTGAAGCCAGCCTGATAATGAAGGATGAACTAGTGTGATT 184 TITITIAAAGAAACAACTIGIAICIAGAGAIGCAGIIIIGATITITIGGGIAAIGIGICI nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuloer; valnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crônis a disease; multiple sclerosis; rheumatoid archititis; ulcerative colitis; andiovascular disorder; wound healing; neurological disease; ds. Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; Human breast and ovarian cancer associated antigen gene SEQ ID 148. 2741 IGTAAICCICTCTTITCCTAITTAGTIGGAIGIGGGITT 2779 TCTAATCCTCCCTTTTTTTAATTTAGTTGGATGTGCTTTT 145 AAF21761 standard; DNA; 1028 BP 27-MAR-2001 (first entry) Homo sapiens. 2641 183 AAF21761; RESULT 13 용 ઠે 원 ò 셤

08-MAR-2000; 2000WO-US005881. 99US-0124270P. (HUMA-) HUMAN GENOME SCI INC. 12-MAR-1999; 21-SEP-2000.

WO200055173-A1.

NPI; 2000-611515/58. P-PSDB; AAB58858.

Rosen CA, Ruben SM;

New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.

Claim 1; Page 592; 1299pp; English.

proteins AAP21614 - AAP22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are equences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; noctropic; or antagonist santiulcer; vulnerary; anticonvulsant; antibacterial; antifilammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifilamsitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists of immune disorders e.g. Addison's disease, allergies, autoimmune of immune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;

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Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                          present invention
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11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                        ATCAAAACCGTCAAATTTTTTTTTTT----TATAATTTAAGAAAGAGTTGGGGAATGAC 5325
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length cDNAs defined in the specification. Where a primer set comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                           cardiovascular disorders such as myocardial ischaemias; wound healing;
                                                                                                 5214 ACAGGIGGGGCCACACTICIGAGGCTGAAAIGIGGCAACCCITTAIC--TAACTIGAA
                                                                                                                    757 acadetraaaagrrccarrrcrgagrgargaaargraacacrrcrrcarcrrraacrrgaa
                                                                                                                                                            ATCABARCTATCAGATTTTTATTTTTTTAAGGAAGGTAAAGTTAGGGACTAGA
                                                                                                                                                                               ATTITITICAGTTGGCCTTTTCAGCTCAGTCATTT-TACGTGTAACGTGGAGATTTGATAG
                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy;
                                                                               Gaps
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           diseases such as cerebral anoxia and epilepsy; and
                                                          1.8%; Score 99.6; DB 3; Length 1028; 70.8%; Pred. No. 1.5e-14; ive 0; Mismatches 64; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; SEQ ID NO 9939; 2537pp + Sequence Listing; English
                                       Sequence 1028 BP; 320 A; 174 C; 199 G; 335 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K,
Otsuki
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA clone (3'-primer) SEQ ID NO:9939.
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Sugiyama T, Wakamatsu
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27-AuG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                  AAH13104 standard; cDNA; 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                   Best Local Similarity 70.8 Matches 177; Conservative
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                   infectious diseases
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            neurological
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complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprisers at strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the sequence and an oligonucleotide comprising a sequence complementary to a copynucleotide which comprises a 3'-end sequence. Where the oligonucleotide which comprises a 1'-end sequence, where the clipsonucleotide which comprises a 1'-end sequence complementary to a copynucleotide which comprises a 1'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in copinate in the primers are useful for synthesising polynucleotides, particularly full-length combas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length combas. The primers allow obtaining of the full-length combas. The primers allow obtaining of the full-length combas. The primers allow obtaining of the full-length combas cashing and and and additional additional additional and additional additional and additional additional and additional additional and additional and additional and and and a sequences; and additional of the compassent collgonucleotides. The sequences and AAH13629 to AAH13623 represent the under an and and are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 482 BP; 170 A; 83 C; 52 G; 170 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 98; DB 4; I
ilarity 70.4%; Pred. No. 2.4e-14;
Conservative 0; Mismatches 65;
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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(HELI-) HELIX RES INST.
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Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; , Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; iehii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 15655; 2537pp + Sequence Listing; English

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification, Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisents to the complementary strand of a polynucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, betterticularly full-length cDNAs. The primers are also useful for the detection and/or disgnassis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13622 represent consent human amino acid sequences; and AAH13622 to AAH13622 represent coligonucleotides, all of which are used in the exemplification of the present invention

Sequence 2148 BP; 639 A; 367 C; 405 G; 737 T; 0 U; 0 Other;

5214 ACAGGTGGGGCCACACTTCTGAGGGCTGAAATGTGGCAACCCTTTATC--TAACTTGAA 5271 9; Gaps 1.8%; Score 98; DB 4; Length 2148; 70.4%; Pred. No. 5.8e-14; ive 0; Mismatches 65; Indels Best Local Similarity 70.4 Matches 176; Conservative Query Match ઠ

1888 ACAGGIAAAAGTTCCATTICTGAGTGATGAAATGTAACACTTCTTCATCTTAACTTGAA 1947 a

ATCAAAACCGTCAAATTTTTATTTT-----TATAATTTAAGAAAGAGTTGGGGAATGAC 5325 5326 ATTTTTGAGTTGGCCTTTTCAGCTCAGTCATTT-TACGTGTAACGTGGAGATTTGATAG 5272 8 ሯ È

2068 TTAAAATTATATTTTGTGTATATAAACATAATTGTGTAAATTGTAATAAATTGTC 2127 5385 요 ठे

2008 AGACTCTAAATTGGCTTCTACAGATCAATAATTTAAATGTAACTAGTTGGGATTTTATAG 2067

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5445 AATTATTAAA 5454

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AATTATTAAA 2137 2128

Search completed: September 15, 2005, 16:13:47 Job time : 2659.83 secs

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Second Company List. Compa	Sequence 1, Sequence 3, Sequence 3, Sequence 3, Sequence 2, Sequence 2, Sequence 1, Sequen	Sequence Seq	Sequence Seq	C E 86.06
Copyright (c) 1939 - 2005 Compagen Ltd. Copyright (c) 1930 - 2005 Copyright (c) 1930	555555555			
September 15, 2005, 12:27:30; Search Line 815.974 Seconds Seconds September 15, 2005, 12:27:30; Search Line 815.974 September 15, 2005, 12:27:30; Search Line 815.974 September 15, 2005, 12:27:30; Search Line 815.974 September 15, 2005, 12:27:30; September 15, 2005, 12:2	1970 5305 1900 1900 2121 1046 1184 7218	9792 9792 9792 9792 9792 1018 1018 1018 1018 1018 1018 1018 101	2687 7997 7997 7997 5798 30310 30310 14507 14507 14507 14507 14507 2010 6112 5191	2044 2226 2226 2226 3646 3646 3665 3686 3686 3686 3686 3686 3686 51039 6727 6727 6727 6727 6727 2432 2432 2432 2432 2432 2432 2432 2
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                                                                      US-09-513-999C-33878

Sequence 33878, Application US/09513999C

Sequence 33878, Application US/09513999C

Sequence 33878, Application US/09513999C

Sequence 33878, Application US/09513999C

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.REG

CURRENT FILING NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 GGGCCGAATAAGTGTTGATTACTCATACCTAGAAGGTGACCTTCCCATTTCTGCCAG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1670 ACCAGTTTGTAGCAACAACTGATAGATTATATTTTGGGAGGCGCCCCCAGTGACTT 1726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.7%; Score 93.8; DB 4; Length 218; Best Local Similarity 70.6%; Pred. No. 1.8e-15; Matches 125; Conservative 0; Mismatches 52; Indels
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 33878
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-999C-33878
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RESULT 2
US-08-726-1/C
US-08-726-1/C
Sequence 1, Application US/08726725
; Patent No. 5773290
; GENERAL INFORMATION:
APPLICANT: Gould, Michael N.
APPLICANT: Chen, Kai-Shun
ITILE OF INVENTION: MAMMARY GLAND-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
IP: 53202-449
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
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RESULT

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3653 AAACCCAGGGCTTTGCACTTGCTAGGCAAGCGCTCTACCACTGAGCTAAATCCCCAAACC 3712
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                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                           ;
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APPLICANT: Kahl Jeffrey Dean
APPLICANT: Kahl Jeffrey Dean
APPLICANT: Kahl Jeffrey Dean
APPLICANT: Wang Tie-Lin
TITLE OF INVENTION: HETEROCYCLIC MODULATORS OF NUCLEAR RECEPTORS
FILE REFERENCE: 38205-3001
CURRENT PELING DATE: 2002-12-20
PRIOR PELING DATE: 2002-12-20
RIOR APPLICATION NUMBER: 60/342,720
PRIOR PELING DATE: 2011-12-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                            Query Match 1.4%; Score 78.8; DB 1; Length 3046; Best Local Similarity 71.2%; Pred. No. 1.6e-10; Matches 104; Conservative 0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.7%; Pred. No. 1.2e-09;
Matches 92; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
NAME/KEY: CDS
LOCATION: (172) ... (1581)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GeneBank U18374
DATABASE ENTRY DATE: 1995-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3733 TTTAAAGACATGGTCTTATATAGTCT 3758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTATTATTTTTGATATGAGGTCT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10329668
Patent No. 6696473
REFERENCE/DOCKET NUMBER: 960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 277-5709
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3046 base pairs
                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-726-725-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Martin Richard
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                       3613 TITTCICCCICTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
LENGTH: 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-329-668-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002 TTTTTTTTTTTTTTTTTTTTTTTTAGGAGCTGGGGACCGAACCCAGGGCCTTGCGCTTG 1943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1942 CTAGGCAAGTGCTCTACCACTGAGCTAAATTCCCAAACCCCTCTTTTGATTTTCTTATAG 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.4%; Score 74.8; DB 4; Length 2010;
Best Local Similarity 67.1%; Pred. No. 1.5e-09;
Matches 106; Conservative 0; Mismatches 52; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08791849A

Sequence 14, Application US/08791849A

Sequence 14, Application US/08791849A

SEQUENCE 101440

TITLE OF INVENTION: Lipid Content in Plant Seed
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Worddperfect 5.1
CURRENT APPLICATION DATA:
PTILING DATA:
SPETIANG DATA:
SOFTWARE: WORDDER: US/08/791,849A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1882 ATAATCATGGTTTCCCCTTTTCTAGTTTCTGCCTTTAA 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3734 TTAAAGACATGGTCTTATATAGTCTAGGCTGGCCTTAA 3771
US-09-809-545A-52/C

Sequence 52, Application US/09809545A

Patent No. 6800455

GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
APPLICANT: White, R. Tyler
TITLE OF INVENTION: SECRETED FACTORS
FILE REPERBNCE: SCIOS.017A

CURRENT APPLICATION NUMBER: US/09/809,545A

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FaetSEQ for Windows Version 4.0

SEQ ID NO 52

LENGTH: 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 January 30, 1997
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                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-809-545A-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: January
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3614 TITCICCCICIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-791-849A-14
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join(3219..3765, 3949..5916, 6009..6151,
6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910, 8078..9297
9480..10162)
                                                                                                                                                                                                                           join(3212.3218, 3766.3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
9298..9479, 10163..10269)
                                                                                                                                                                                                                                                                                                                                         join(3194..3218, 3766..3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3645 TGAGGACCAAACCCAGGGCTTTGCACTTGCTAGGCAAGCGCTCTACCACTGAGCTAAATC 3704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/08135511
Patent No. 5558999
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Methods for Using Them
NUMBER OF SEQUENCES 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Score 74.2; DB 2; Length 13011; 69.9%; Pred. No. 8.2e-09; tive 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE: 13-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10855 CCAACCCCAGCTTTTCTCTTTTT 10877
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NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31, 298
REFERENCE/DOCKET NUMBER: 18748/175
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3705 CCCAAACCACCCCCCCCTTTT 3727
                                                                                      MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
REATURE: rat (Rattus norvegicus)
                                                                      linear
E: DNA (genomic)
LENGTH: 13011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: (202)672-5399
TELEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.9
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-135-511-31/c
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
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                                                                                                                                                                                                                           LOCATION:
LOCATION:
LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                              3600 CTTCAGTGGATTTTCTCCCTCTTTTTTTTTCCCCCAGAGCTGAGGACCAAACCCA 3659
                                                                                                                                                                                                                                                                                                                                                                                                           4861 GGGCCTTGCGCTTGCTAGGCAAGTGCTCTACCACTGAGCTAAATCCCCAGCCCCAGCACT 4802
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08187453
Sequence 31, Application US/08187453
Patent No. 5753431
GENERAL INFORMATION:
APPLICANT: Chiang, John
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                 Query Match 1.3%; Score 73.6; DB 1; Length 7970; Best Local Similarity 73.4%; Pred. No. 8.5e-09; Matches 94; Conservative 0; Mismatches 34: Tndela n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: HEW PC compatible
COMPUTER: A PETERICALION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/187,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COlin G
REGISTRATION NUMBER: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G
REGISTRATION NUMBER: 131,298
REGISTRATION NUMBER: 18748/188
TELECOMMUNICATION INDERE: 18748/188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 7997 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-135-511-31
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (202) 672-5300
(202) 672-5399
                                     LENGTH: 7970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3720 CCCCTTTT 3727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4801 AAAGTTTT 4794
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20007-5109
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4948 CTACAGCACTAAAGTTTTTTTTTTTTTTTTTTTTTTTTCAGAGCTGGGGACCGAACCCA 4889
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                                                                                                                                                                                                                                                                                                                                       TTCCCCCAGAGCTGAGGACCAAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3600 CTTCAGTGGTGGATTTTCTCCCTCTTTTTTTTTTCCCCCAGAGCTGAGGACCAAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOLESTEROL 7ALPHA-HYDROXYLASE EXPRESSION AND CHARACTERIZATION OF ITS REGULATORY ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                                                                                                                                           Length 7997;
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                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MESHINGSON
STATE: D.C.
COUNTRY: USA
ZUP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/562,985A
FILING DATE: 27-NOV-1995
CLASSIFICATION: 435 STONONEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REGISTRATION NUMBER: 31,298
REGISTRATION INFORMATION:
TELEFHONE: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: O00136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERICIS:
                                                                                                                                      Score 73.6; DB 1;
Pred. No. 8.6e-09;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-562-985A-7/C

Sequence 7, Application US/08562985A

Patent No. 5821057;
GRNERAL INFORMATION:
APPLICANT: CHIANG, John Y.L.
APPLICANT: STROUP, Diane
TITLE OF INVENTION: AN ASSAY FOR AGENTS THAY
TITLE OF INVENTION: CHOLESTEROL 7ALPHA-HYDR
TITLE OF INVENTION: CHOLESTEROL 7ALPHA-HYDR
TITLE OF INVENTION: CHARACTERIZATION OF ITS
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                       3600 CTTCAGTGGTGGATTTTCTCCCTCTT
i MOLECULE TYPE: DNA (genomic)
US-08-187-453-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3%;
                                                                                                                                           1.3%;
ilarity 73.4%;
Conservative
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Best Local Similarity 73.4'
Matches 94; Conservative
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                           Query Match
Best Local Similarity
Matches 94; Conserv
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1732 éceaegécaagrecréraccacréaecraaarcrécaaccereaagecerérrerrer 1791
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1.3%; Score 69.6; DB 3; Length 2432;
Best Local Similarity 64.0%; Pred. No. 4.8e-08;
Matches 105; Conservative 0; Mismatches 59; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTAL: 0.0...
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
                                                                                             3684 GCTCTACCACTGAGCTAAATCCCCAAACC 3712
                                                                                                                                                            7701 GCTCTACCACTGAGCTAAATCCCCAGCCC 7729
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
APPLICANT: Chang, Ming-Shi
APPLICANT: Chang, Ming-Shi
NUMBER OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08795445A
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: I
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124..1326
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FEATURE:
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US-08-974-022-1
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US-08-795-445A-1
                                                                                                                                                                                                                                                          RESULT 11
US-08-974-022-1
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Patent No. 6780510

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Owens, Gary

APPLICANT: Owens, Gary

APPLICANT: Owens, Gary

TITLE OF INVENTION: Identification of a Smooth Muscle Cell (SMC) Specific Smooth Musc

TITLE OF INVENTION: Identification of a Smooth Muscle Cell (SMC) Specific Smooth Musc

TITLE OF INVENTION: Models 1.03

CURRENT PELICATION NUMBER: US/09/600,319

FRIOR PELICATION NUMBER: PCT/US99/01038

PRIOR PILING DATE: 1999-01-15

PRIOR PILING DATE: 1999-01-15

PRIOR PILING DATE: 1999-01-16

NUMBER OF SEQ ID NOS: 3

SOUTHARE: PatentIn version 3.0

SEQ ID NO 3

LEASTH: 16011

MANDER OF SEQ ID NOS: 3

MANDER OF SEQ ID NOS: 3

SEQ ID NO 3

LEASTH: 16011
                                                                                                                                                                                                                                         US-09-600-319-3/C

| Sequence 3, Application US/09600319 |
| Sequence 3, Application US/09600319 |
| Patent No. 6780610 |
| GENERAL INFORMATION: |
| APPLICANT: Owens, Gary |
| APPLICANT: Owens, Gary |
| APPLICANT: Wadsen, Cort |
| TITLE OF INVENTION: Identification of a Smooth Muscle Cell (SMC) Specific Smooth Musc |
| TITLE OF INVENTION: Myosin Heavy Chain (SM-MHC) Promoter/Enhancer |
| FILE REFERENCE: 00241-03 |
| CURRENT APPLICATION NUMBER: PCT/US99/01038 |
| PRIOR FILING DATE: 1999-01-15 |
| PRIOR FILING DATE: 1999-01-16 |
| PRIOR PILING DATE: 1999-01-16 |
| NUMBER OF SEQ ID NOS: 3 |
| SOFTHARE: PATENTIN Version 3.0 |
| CONTINUED OF SEQ ID NOS: 3 |
| CONTINUED OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14537 ATTITITITITITITGGITCTTTTTTCGGAGCTGGGGACCGAACCCAGGGCCTTGCGCT 14478
   4888 GGGCCTTGCGCTTGCTAGGCAAGTGCTCTACCACTGAGCTAAATCCCCAGCCCCAGCACT 4829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3612 ATTTTCTCCCTCTTTTTTTTTTCCCCCAGAGCTGAGGACCAAACCCAGGGCTTTGCACT 3671
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Pred. No. 1.6e-07;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 16011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71.2; DB 4;
Pred. No. 6.4e-08;
0; Mismatches 28
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Best Local Similarity 86.5%;
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Rattus norvegicus US-09-600-319-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 75.9
Matches 88; Conservative
                                                               3720 CCCCTTTT 3727
                                                                                                                           4828 AAAGTTTT 4821
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                                                            δ
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Sequence 1, Application US/08974186
Patent No. 6284740
                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WINTER, ROBERT B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 64.0
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
124..1326
Thousand Oaks
                    California
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                         91362-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-795-447A-1
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                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1672 TITATITATITITIATICITITITICGGAGCTGGGGGCCGAACCCAGGGCTTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3733 TTTAAAGACATGGTCTTATATAGTCTAGGCTGGCCTTAAACTCA 3776
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                                                                                                                                                                                                                                                                                                                                                           OPERATION SYSTEM: PC-DOS/ND-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFTATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/577,788
APPLICATION NUMBER: 08/577,788
FILING DATE:
NAME: WINCET, RODERT B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER STICS:
LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
              GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITTLE OF INVENTION: OSTEOPROTEGERIN
WUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
MUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
                                                                                                                                                                   ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 105; Conservative
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124..1326
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Patent No. 6284485
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; LOCATION:
US-08-795-445A-1
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: ABC TOWN:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/974,186

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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3613 TITICICCCTCTTTTTTTTTCCCCCAGAGCTGAGGACCAAACCCAGGGCTTTGCACTT 3672
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1.3%; Score 69.6; DB 3; Length 2432;
Best Local Similarity 64.0%; Pred. No. 4.8e-08;
Matches 105; Conservative 0; Mismatches 59; Indels 0
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APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08795446B
Fatent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES:
ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICATION NUMBER: 08/577,788
        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WINEE, ROBERT B.
REFERENCE/DOCKET NUMBER: A-:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: Winter, Robert B.
REFERENCE FOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: cDNA
FRATURE:
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LOCATION:
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                                                                               Length 2432;
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                                                                                                           59; Indels
                                                                              Score 69.6; DB 3;
Pred. No. 4.8e-08;
0; Mismatches 59;
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ne : 827.974 secs
                                                                              1.3%;
                                                                                              Best Local Similarity 64.0
Matches 105; Conservative
                           CDS
124..1326
MOLECULE TYPE: CDNA
              ; FEATURE:
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; LOCATION:
US-08-795-446B-1
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Run on:

Scoring table:

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Minimum I Maximum I

Database

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1324 1189.2 1189.2 542.6 215.8 181.6

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Score

Result Š. 93, A 118,

301 AGCCGCCGCTCTCTGGGGCTCCTCTGCCGGGAATCGGACTGCAGTACCCACTCCG 360 361 TGGCTGGGCAAGGCGAAGCCGTTAGACCTCGGATCCAGCCTGACGCTGACGTACCCACTCCG 420		1321 AAATCCACCTTCGTATGAAACGGCTAGAATTCCTCCAGGCTAACGAAGGGCAAGAGT 138 1321 AAATCCACCTTCGTATGAAACGGCTAGAATTCCTCCAGGCTAACAAAGGGCAAGAGT 138 1321 AAATCCACCTTCGTATGAAACGGCTAGAATTCCTCCAGGCTAACAAAGGGCAAGAGT 138 1381 TACCCACCCCTGACCAAGATAATGGCTATCATAGCCTGGAGGAACATAACCTTCTCC 144 1381 TACCCACCCCTGACCAAGATAATGGCTATCATAGCCTGGAGGAAGAACATAACCTTCTCC 144 1381 TACCCACCCCTGACCAAGATAATGGCTATCATAGCCTGGAGGAGGAACATAACCTTCTCC 144
8	1	6 4 6 6
71.6 1.3 2145 17 US-10-108-260A-2352 Sequence 2352, Ap 71.6 1.3 21688 21 US-10-419-296-31 Sequence 31, Appl 71.6 1.3 21688 21 US-10-621-911A-9 Sequence 9, Appli 51.6 1.3 21688 21 US-10-646-390A-9 Sequence 9, Appli 51.4 1.3 344 9 US-09-917-800A-278 Sequence 278, Appli 51.4 1.3 344 17 US-10-191-803-998 Sequence 278, Appli 51.2 1.3 1201 18 US-10-307-817-613 Sequence 613, Appli 51.2 1.3 16011 14 US-10-307-817-613 Sequence 613, Appli 51.3 16011 14 US-10-087-132-135 Sequence 105, Appli 51.3 16011 14 US-10-087-132-135 Sequence 115, Appli 51.3 2015 9 US-09-917-800A-473 Sequence 3172, Appli 51.3 2015 9 US-09-917-800A-473 Sequence 715, Appli 51.3 2015 9 US-09-934-71 Sequence 715, Appli 51.3 2015 9 US-10-386-934-71 Sequence 715, Appli 51.3 2013 9 US-10-332-281-115 Sequence 34, Appli 51.3 2181 19 US-10-75-432-3 Sequence 66, Appli 51.3 2161 14 US-10-175-533-66 Sequence 66, Appli 51.3 2161 24 US-11-099-266-66 Sequence 144, Appli 51.3 2161 24 US-11-388-934-144 Sequence 144, Appli 51.3 2161 24 US-11-388-934-144	RESULT 1 RESULT 2 RESULT 2	

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141 GGATTGGACCACCACACACACACACACACACACACACACA

141 THINGOACTGCATTAGTAGTCCATATTTTTTGGGAACCCCATTTCTGTGTA 141 THINGOACTGCATTAGTAGTCCCGG 1800 141 THINGOACTGCATTAGTAGTCAGTCAGTCAGTCAGTTTAGGAACAA 1800 141 THINGOACTGCTTTAGGAACTCAGTTTAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACAACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACAACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGGAACACTTCAGGAACAACACTTCAGGAACAA 1800 1801 GGAATGGGCTAGTTTAGACACACTTCAGAACACACTTCATT 1920 1801 GGAATGGGCTAGTTTAGACACACTTCAGTTT 1920 1801 GGAATGGGCTAGTTTAGACACACTTCAGTTT 1920 1801 GGAATGGGTCAGTTAGACACACTTCAGTTT 1920 1801 GGAATGGGTCAGTTAGACACTTCAGACACACTTCAGACACACTTCAGACACACAC	RESULT 2 US-10-650-482-1 US-10-650-482-1 US-10-650-482-1 US-10-650-482-1 Subdication No. US20040142345A1 Subdication No. US20040142345A1 GENERAL INFORMATION: APPLICANT: Non. David APPLICANT: Non. David TITLE OF INVENTION: METHODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN elF2alpha-S TITLE OF INVENTION: PHOSPHATASE SUBUNIT FILE REPERENCE: 5986/11/12-US1 CURRENT APPLICATION NUMBER: US/10/650,482 CURRENT FILING DATE: 2003-08-28 FRIOR PILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 10 SEQ ID NO 1 SEQ ID NO 1 LENGTH: 2942
	441 TGGATCAGGTGCTTGGTTTGTTCAGTTAGCGTCCTGTTGTGCATGGTTGAGGTAAT 4500 441 TGGATCAGGTGCTTGGTTTGTTCAGTTAGCGTCCCTGTTGTGCATGGTTGAGGTAAT 4500 441 TGGATCAGGTGTGTTTGTTCAGTTAGCGTCCCTGTTGTGCATGGGTGAGTAAT 4500 4501 GTGTTACCAGTTCTTTAGTGGTTACATGCAAAAGAGAGCTCTCTGAGTCGGGTGTAGT 4500 4501 GTGTTACCAGTTCTTTAGTGGTTACATGCAAAAGAGAGCACTCTGAGTCGGGTGTTG 450 4501 GTGTTACCAGTTCTTTAGTGGTTACATGCAAAAAGAGAGACCTCTCAGTCGGTGTTG 450 451 GATGAGCTTTCCAGACCTGGCAGGGTAAACTACCTCAGTTTATAATGTCCCTGGTTATTT 4620 4621 CCGTTTGATGTGATCTAAGGTCTGCCTCAGTGGTGATTATAAATGTCCCTGGTTATTT 4620 4621 CCGTTTGATGTGATCTAAGGTCTGCCTCAGTGGTGATGTTCATCCACACACA

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TYPE: DNA ORGANISM: Homo sapiens	24.2%; Score 1324; DB 19; Length 2942; rrity 72.5%; Pred. No. 0;	85-75 25-75 25-75	ACGICTICCTTCCTAGCCGGGATCTAACCGCGTTCGCCACCCACCTCCTCCTTCCT	TOGGCCGTCCGGTGCACACTCGTTGCGGAAGCCGCCGCTCTCTGGGCCCGCTCTCTGCCGGGGAAGCCGCCGCTCTCTGGGGCCGCTCTCTGCGGCGGGGGGGG	CGCGGGAATCGGACTGCAGTACCCACTCCGTGGCCAGAGGCGGAGACTGTGTAGACC	TCGGATCCAGCCTGACGCCGCTGAGCTCTGTCCTCCTCCTCTTGAGAGCCGCCCCTCTTGAGAGCCGCCCCTCTTGTCTTGAGAGAGCCGCCCCTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	ANG-GRANAGAGAGAGAGAACGCACAGAGACCCCGGAACCCTGGCCCTCGGCTG ANG-GRANAGAGAGAGAGAGAACGCACAGAGACCCCGGAAGCCCCTCGCCCTCGGCTG ANG-ANANAAGAGAGAGAGACGCGGAAACGCGGAAACGGCTTGGCCCTCGGCCG ANG-ANANAAGAGAGAGAGCCGGGGACAGCGGAAACGGCTTGGCCCTCGGGCG	510 GGCTCCTGGTTCCGGCTGCCCTTCCTTCGGCGATCGCACCTGCTGCTTCGGAGTTC 566 [CGCCGCCTTCCTCTCGAAAATCCCGGGAACTCCGCTCTGCCC		CTATTCCAGAAGCTGCTGCTTTGGAGCCAGCTTTCCGGGGGCCTGATTCCTACCAGATGG T	CTAGATTTTGCCGCAAGTTACAGCGCCCTGAGAGCTTCGAGAGGACGCGGAGGAATCTGACTTAGAGGACCTGAAGGAGCCTGAAGGACGAGAAAGGAAAACAGCG		GTCGTCAGTACTCTTGCCTAGAGGAGGACTCCAGTGGCAGTGCTCGTCCTCAGA	GSICACCAGICCCTITATITGGCIAGAGGGGATTCCACTGGCAATACTCGCCCCCCAGACTTTCCT	CCTAAAATTGGAGCTTAAGGCCAAGGGAAGTGCTTTGGACCCTGCAGGCTTTTCT CCTGGAGCAGCAGCAGCTGGAGTTGCTGCCCAGTAGCCTTCAAGCTGATCTAGT		HGAL CAN

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TAATGGCTATCATAGCCTGGAGGAACATAACCTTCTCCGGATGGACCCACAACATTG 1459
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               TITCAACCCTCTGTCAGTCGGCGATCGCAAGCAGGCTCTTCTAAGTTCCCGACGCCTCTT
                                                                GGCCCGGAAAACTCCGGGAACCCCCACACTGCTTTCCTCTGCCCAGCCCGGAGACTCGGGTC
                                                                                                            CAGAAGTCTCTGAGTTACACTGCGGCTGGACTCTTCGCGAAGACTCGCGTCGTCAGTACT
                                                                                                AGGTACTGGACCAAATTGCTTTCTCAGCTCCTTGCCCTGCTCCCTAGCCTATTCCAGAAG
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TTCCGGCTGCCCTTCCTTCGCGATCGCACGCCTGCTCTTCGGAGTTCCCGCCGCCTTCC
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                                                                                                                         TATCAAGAGAAAAAGGTAACCTTCCTGGAAGAAGTTACTGAGTATTATATAGGGGGAGTATTATATAGTGGTGA
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                         AGTGGCCTTCTCGGCCATCATACCTTACTTTGTAAGGCCCAGCTGTTAGAGAGCCA
                                       AGAAGATAATTGTCCAGGCTGTGGGCTGGGTGAGGCTCTTGCTGGAGAAAGATACACCCA
                                                                                         AATTCAAGAAACAGAAGTTGCCATTGGCTACTGCTTGGCCTTTGAGCACAGAAAAAT
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; Sequence 166, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT FAPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 168
; LENGTH: 2324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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; Pred. No. 0;
4; Mismatches
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Best Local Similarity 75.3%;
Matches 1642; Conservative
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GTGCTTTT 2798
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; ORGANISM: Homo
US-09-925-299-168
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US-09-925-299-168
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Db 2199 AGCTGTCCTTTGACATTTTTT 2220	BESTIAN 1885
	113 COLOCITATION CONTRICTOR CONTRIBUTION

Db 1779 TGAGGCCCATACTTCTTGTAAGTGCGGCGCCAGGAGCCAGGAAGTGT 1838 Qy 2270 TCCAGGCTGTGGGCTGAGCTCTTGCTGGAGAAGAACACCCATATCAAGAAA 1838 Qy 2330 TCCAGACTCGGTAACATTCTTGCAGGAAACACACACACAC	RESULT 5 REPLICATION NO. US20040053248A15 REPLICATION NO. US20040053248A161 RULD 6 RULD 6
1163 GAGCAGCGCTGGAGGTGGCCAGTTTCCGAACACTAACCCCAGAGGCTGCTA 1222	1613 CCACACTAATGCAACTGACCTCTCAGATACAGAGAGAGACCTTCCTGTTTCTCCCAGACC 1672

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1116
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                                                                                                                                                                                                                                                                                                                997 AGTTGCTGCCCAGTAGCCTTCAAGCTGGTCTAGTCTCCCACCGAGAACTTGACTCTTCAT 1056
                                                                                                                                                                                                                                                           177 GAAGTGCTTTGGACCCTGCAGCACAGGCTTTTCTCTTTAGAGCAGCAGCTGTGGGGAGTGG 236
                                                                                                                                                                                                                                                                                                                                              237 AGCTGTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTCGC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 CCTCTGGGCTTCTAAACATTCAACGCATAGACAATTTCAGTGTGTGGTATCCTATTTGCTGA 356
                                                                                                   936
                                                                                                                                                  117 Aggaggggarccacrigggaracregeeeeceaaaccraaaarrggagerraaggeeaagg 176
                                                                                                                                                                                                         937 AAAGAGCTTTAGACTCTGCAGCGCCCACTTTCCTCCTGGAGCAGCAGCTGTGGGGAGTGG 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 ACCCTTCCTACCTGGACTGCTTTTCTAGGCTAGAAGTCAGCTATCAGAAACAGTGATGGA 416
                                 878 AGGAGGGACTCCAGTGGCAGTGCTCGTCCTCAGA-CTGGAAGTTAAACTCAAGGCCCAGG
818 TIACACTGCGGCTGGACTCTTCGCGAAGACTCGCGTCGTCACTACTCTTGCATTGGCTAG
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US-09-917-800A-1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176 GGTGGCCAGTTTGTGGGTTTCCGAACAC-TAACCCCAGAGAGCTGCT 1221
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APPLICANT: Derter, Mark
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANTON: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US 60/220,040
PRIOR APPLICATION NUMBER: US 60/220,040
PRIOR PILING DATE: 2000-01-02
PRIOR PILING DATE: 2001-05-11
PRIOR PLICATION NUMBER: US 60/290,645
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Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
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APPLICANT: AZIZ, NATAGERIA
APPLICANT: ZIOTHIK, ALDERT
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
TITLE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARES: Patentin version 3.2
SEQ ID NO 3997
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                      2190 GAGGTCACAGTGGCCTTCTCGGCCATCATACCTTACTTTCTTGTAAGGCCCAGCTGTTA 2249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAACGAATTCAAGAAACAGAAGTTGCCATTGGCTACTGCTTGGCCTTTGAGCACAGA 2489
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TCTGGCAGCTGTGGTGTAGGGA---GCTGTCAGGAGGACCCCTTCCGGAGACCCCCGAC 2015
                                                                                                                                                                                                       ---TIGIGGAACTCTTTCTGTCA---TTCTGAGGACCCCTACAACCTTTAAATTTTAAG 2129
                                                                                                                                                                                                                                                                                                             2130 GCTCCTTTTCAACCGTCAGGGAAGAATTGGAAAGGCCGTCAGGACTCAAAGGCCTTTTT 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2250 GAGAGCCAAGAAGATAATTGTCCAGGCTGTGGGCTGAGGCTTTGCTGGAGAAAGA 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2310 TACACCCATATCAAGAGAAAAAGGTAACCTTCCTGGAAGAAGTTACTGAGTATTATATA 2369
                                                                                           481 GAGTCCATTGTGGCCATTTCTGAGTGTCACACCTTACTTTCTTGTAAGGTGCAGCTGTTG 540
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                                                                                                                                                                                                                                                           361 ACTGTGGGAACTTCATTCTGTTAATTCTGGATGGACCCCTACAACCTTTAAATTTTAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 GAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTCTCAAGGAA 840
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3.9%; Score 215.8; DB 22; Length
Best Local Similarity 73.4%; Pred. No. 6e-48;
Matches 343; Conservative 0; Mismatches 117; Indels
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CORGANISM: Homo Sapiens
US-10-756-149-3997
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GENERAL INPOGNATION:
GENERAL INPOGNATION:
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
TITLE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT APPLICATION NUMBER: US/09/783,590
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12337
                                                                                                                                                                                                                           2503 ATAGACTGAGGATCGAGTCAAAGGACTTACTGTTGTACAGCAATGTTAAGA--AGTGAAC 2560
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                                                                                                                                                                            282 crrcaagcaaacargrrrcaaaggacrraargrrrrcgagcaargrraagargarrcgac 341
  102 ATAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTACATAAGCGGTGATGAGGATCGAAA 161
                                                                                        162 AGGACCATGGGAAGAATTTGCACGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAAC 221
                                              2390 AGGACCATGGGAAGAATTTGCAAGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAAC
                                                                                                                                     2450 AGAAGTTGCCATTGGCTACTGCTTTGGCCTTTGAGCACAGAGAAAAA----ATGTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-12337
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NAME/KEY: misc feature
LOCATION: (1)
CTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (4)
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Weeley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
TITLE OF INVENTION: WICKIEL ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WINGSCHE AND FAT DEPOSITION
TITLE OF INVENTION NUMBER: US 60/1039/963, 965
CURRENT APPLICATION NUMBER: US 60/103, 678
PRIOR FILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-17
SEQ ID NO 2096
IENGTH: 399
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                            11;
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                                                                                                                                                                                      5121 GGCAGGCAGGCAGGCATGCTGGTTCTAGTTGAATACACATTC-AAGTCTTGCAGTG
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75.8%; Pred. No. 1.7e-38;
tive 0; Mismatches 69; Indels
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3.1%; Score 170.8; DB 9; Length
Best Local Similarity 79.1%; Pred. No. 1.3e-35;
Matches 231; Conservative 0; Mismatches 52; Indels
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US-09-983-965-2096
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Patent No. US20020137160A1
Best Local Similarity 75.89
Matches 388; Conservative
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US-09-983-965-2096
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                                                                                                                                                                                                                                                                         Score 99.6; DB 9; Length 1028; Pred. No. 8.9e-16; 0; Mismatches 64; Indels 9.
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 148
LENGTH: 1028
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Best Local Similarity 70.8%;
Matches 177; Conservative (
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Best Local Similarity 70.8%;
Matches 177; Conservative
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US-09-925-298-148
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US-10-102-806-148
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                                                                                         92 GGGATCTAGTGCAGATGAAGCAGAGAGTCTCAAACTGTGGAACTCCCATTCTGTAATTCTG 141
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                                                         2042 GGAACCGAGTGCAGATGAAGCAGAGAATCTTAAATTGTGGBACT-CTTTCTGTCATTCTG
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US-09-925-298-148

i Sequence 148, Application US/09925298
; Sequence 148, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; PILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
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PUBLIcation No. US20030073623A1
GENERAL INFORMATION: US20030073623A1
TITLE OF INVENTION: NOVEL NUCLBIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 1999-01-07-30
PRIOR FILING DATE: 1999-01-20
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2.0%; Score 109; DB 10;
Best Local Similarity 71.6%; Pred. No. 1.3e-18;
Matches 187; Conservative 0; Mismatches 65;
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 36363
LENGTH: 421
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ORGANISM: Homo sapiens
US-09-918-995-36363
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Sequence 148, Application US/10102806

Publication No. US20030054421A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PLC1

CURRENT APPLICATION NUMBER: US/10/102,806

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

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PRIOR PLING D
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Pred. No. 8.9e-16;
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                                                                      937 TIAAAATTATATTTGTGTATATAACATAACTAATCTGTAATTGTAATAATAATATTTGC 996
877 AGACTCTAAATTGGCTTCTACAGATCAATAATTTAAATGTAACTAGTTGGGATTTTATAG 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: PastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 162
LENGTH: 2148
                                                                                                                                                                                                                                                                                                              APPLICANT: Ward, Neil Raymond
APPLICANT: Ward, Neil Raymond
APPLICANT: Wandy, Christopher Robert
APPLICANT: Ran, On
APPLICANT: White, Jonathan
APPLICANT: White, Jonathan
APPLICANT: Rayner, William Nigel
APPLICANT: Rayner, William Nigel
APPLICANT: Rayner, William Nigel
APPLICANT: Kringeman, Susan Mary
APPLICANT: Kringe, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 53262000100
CURRENT FILIG DATE: 2002-06-12.
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US-10-131-827-8849
S. Sequence 8849, Application US/10131827
Publication No. US2004000479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
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; Sequence 162, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
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Matches 176; Conservative
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APPLICANT: 15, NGOC TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR RILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 8849
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APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gane Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REPERENCE: 44921-5038-08
FILE REPERENCE: 4001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-11-02
PRIOR PRIOR DATE: 2000-11-05
PRIOR PRILING DATE: 2001-05-11
PRIOR PRILING DATE: 2001-05-11
PRIOR PRILING DATE: 2001-05-12
PRIOR PRILING DATE: 2001-05-15
PRIOR PRILING DATE: 2001-05-16
PRIOR PRILING DATE: 2001-05-16
PRIOR PRILING DATE: 2001-05-16
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Patent No. US20020119462A1
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Woodward, Robert
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Best Local Similarity 70.4<sup>†</sup>
Matches 176; Conservative
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2128 AATTATTAAA 2137
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ORGANISM: Homo sapiens
US-10-131-827-8849
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US-09-917-800A-1399
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Search completed: September 16, 2005, 10:40:03 Job time : 3240.64 secs

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and is derived by analysis of the total score distribution.
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.jp, VRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="cerebellum"
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TFLEEVTBYYISGDEDRKGPWEEFARDGCRFOKRIQETEVAIGYCLAFEHREKMFNRL
                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="C230093D15"
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/db_xref="GI:26339692"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 2731)

S Adachi,', Aizawa, K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashida,K., Hayashida,K., Hayashida,K., Hayashida,K., Maratsu,N., Hiramoto,K., Hiramoto,H., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Satoh,H., Sakai,C., Sakai,K., Shinagawa,A., Shiraki,T., Sano,H., Saaaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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              CD560629 B0416D08-
BE914017 601665429
BI713435 ic88e10.y
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                     AKO49028 2731 bp mRNA linear HTC 03-APR-2
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:C230093D15 product:hypothetical protein,
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nahi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsaxaki, Y., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sagabe, Y., Taqami, M., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Taya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Taya, T., Yasunishi, A., Direct Submission

AL Submitted (16-APR-2002) Yoshinde Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Group, RIKEN Genomic Sciences Center (GSC), RIKEN Gana, Tayana (B-mail:genome-reseges.riken.jp, Vokohama 1981.ttte; 1-7-2. Suchir. Centumi-ku, Yokohama, Hay-503-9216,
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RGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSES
DVEQDSEGLHLWNSFHSVDPYNPQNFTATIQTAARIAPRDPSDSGTSWSGSCGVGSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="spinal cord"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
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TFLEEVTEYYISGDEDRKGPWEEFARDGCRFÇKRIQETEVAIGYCLAFEHREKMFNRL
RIBSKDLLLYSNVKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="C530022L24"
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/db_xref="G1:26350137"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonkazaki,Y., Bihikwaw,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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Nature 420, 563-573 (2002)
6 (bases 1 to 2619)
7 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                     GTCTCATTAGAAACACCCCAATAATGAAGAATCTCTTATCTGTAATCTCTCTTT
                                                                                                                                                            CCTATITAGTTGGATGTGGGTTTTTGTCTTTTTGAGAGGGTCTCACTGCATAATTCTGTTT
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hayashida, K., Tandani, K., Ishii, Y., Itoh, M., Kagawa, T., Hirozane, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Sano, H., Sasaki, D., Shibata, K., Shinada, K., Shiraki, T.,
Sano, H., Sasaki, D., Shibata, K., Shinada, R., Shiraki, T.,
Takeda, Y., Tagami, M., Tagawa, A., Takahshi, F., Takaku-Akahira, S.,
Takeda, Y., Tanamaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A.,
Direct Submission
Submitted (16-Apr-202) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-reseascriken:jp,
UKL:http://genome.gsc.riken:jp, Tel:81-45-503-9222,
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/db_xref="taxon:10090"
/db_xref="taxon:1001"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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LRGREESAAPTVQKSISSLRLDSSEDLVVSSLDWLEEGLQWQCSSDLELKIKAQERA
LDSAAPTFLEQQLWGYPLLPSSLQGALVSHRELDSSSSGPLSVQSLGNFKVVSYLLN
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NPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPV
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/db_xref="G1:26352129"
/translation="METGTHRARKRPGPRLGSWFRLPFLRRSHACSSEFPPPSSRQNP
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Encyclopedia Project of Genome Exploration Research Group in Rike
Encyclopedia Project of Genome Exploration Research Group in Rike
Bioxicon of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
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Best Local Similarity 98.5%; Pred. No. 1.1e-307;
Matches 1325; Conservative 0; Mismatches 15;
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/strain="C57BL/6J"
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                                                                                                                                               2457
                                                                                                                                                                                                        2564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTC 03-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930040107 product:hypothetical protein, full insert
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1342)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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        GAAACAGAAGTTGCCATTGGCTACTGCTTGGCCTTTTGAGCACAGAGAAAAATGTTTAAT
                                                                                                                                                                                                     AGACTGAGGATCGAGTCAAAGGACTTACTGTTACAGCAATGTTAAGAAGTGAACAGCC
                                                                                                                                                                                                                                                     2458 AGACTGAGGATCGAGTCAAAGGACTTACTGTTGTACAGCAATGTTAAGAAGTGAACAGCC
                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase II Team and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Qy 1569 AGTCTGTTTTGTGAATTACCCGTGG 1593 Db 1318 AGTCTGTTTTGTGAATTACCCGTGG 1342	Z Ö z	mouse) Chordata;	; Rodentia; Sciurognathi; Muridae ; nci.nih.gov/. s of Health, Mammalian Gene Colle	_	CDNA LIDRARY Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be		FEATURES LOCATION/QUALITIETS SOURCE 1 .871 /roganism="Mus musculus" /mol_type="mrNA"	/strain="Press"" /db_xref="texps"" /clone="IMAGE:6395811" /lab_host="DH10B (T1 phage-resistant)"	/Clone_inloan_Cafe_Cos4" /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by life mochael ansert size 1.6 kb. Constructed by life	ORIGIN ONEY MATCH 15.1%: Score 828.2: DB 5: Length 871:	Similarity 97.9%; Pred. No. 2.2e-196; 9; Conservative 0; Mismatches 18; Indels 0; Gaps	Qy 4463 TICAGTIAGCGICACCTGTTGTGCATGGTTGAGGTAATGTGTTACCAGTTCTTTAGTGGT 4522	4523 TACATGCACAAAAGAGACCTCTGAGTCGGGTGTGGGATGAGCTTTCCAGACCTGGCA	DB 61 TACATGCACAAAAGAGAGAGACCICTGAGTGGGGGGGGGG	121 GGGTAAACTACCTCAGTTTATAATCTCCCTGGTTATTTCCGTTTGATGTGATCTAAGGTC	Oy 4643 TGCCTCAGTGGTGATGATGTTCATCCACAAGGTTAGTAAGAGTGCACAACAAAA 4702 181, TGCCTCAGTGGTGATGATGTTCATCCACAAAGGTTAGTAAGAGTGCACGACAAAAA 240	Qy 4703 CGTTGGTCTTATTTTGAGAACCCCCATTTCTGTGTATTTTATGCACCTGCCTTTAGTGA 4762	4763 ACTCCAGAGTGCATTAAAGAGTCTGGTTTAGTGCGGAATGGGCTAGTTTAGAAGCT
dy 490 AGCGGCCTGGCCTCGGCTGCTCCGGCTGCCCTTCGGCGATCGCACG 549 Db 242 AGCGGCCTGGCCTGGCTGCTCCTGGTTCCGGCTGCCCTTCCTTCGGCATCGCACG 301	S50 CCTGCTCTCGGAGTTCCCGCCGTTCCTCGACAAATCCCGGGAACTCCGCTCTGC 609	670 GCCTATTCCAGAAGCTGCTGCTTTTGCAGCCTTTTCCGGGGGCCTGATTCCTACCAGAT 729	730 GGCTAGATTITGCCGCAAGTTACAGCGCCCTGAGAGCTTCGAGAGGAGGAGGAATCTG 789 	790 ACGCTCCCACGGTGCAGAAGTCTCTGAGTTACACTGCGGCTGGACTCTTCGCGAAGACTC 849	850 GCGTCGTCAGTACTCTTGCATTGGCTAGAGGGACTCCAGTGGCAGTGCTCGTCA 909	910 GA-CTGGAAGTTAAACTCAAGGCCCAGGAAAGAGCTTTAGACTCTGCAGGGCCCACTTTC 968 	969 CTCCTGGAGCAGCAGCTGTGGGAGTTGCTGCCCAGTAGCCTTCAAGCTGGTCTA 1028 	1029 GTCTCCCACCGAGAACTTGACTCTTCATCCTCTGGGCCTCTGAGGGTTCAGAGGTTAGGT 1088 	1089 AATTICAAGGTAGTITCCTAICTCCTGAACCCTTCCTGCACTACCTTCCCCGGTTA 1148 	1149 GGGCTGCGCTGTCAGAGCAGCGCTGGAGGTGGCCAGTTTGTGGGTTTCCGAACACTAACC 1208	CCAGAGAGCTGCTATCTTTCTGAAGATGGTTGTCACCCTCAGCCGTTGCGGGCAGAGATG	958 CCAGAGAGCTGCTATCTTTCTGAAGATGGTTGTCACCCTCAGCCGTTGCGGGCAGAGTG 1017 1269 TCGGCAACCGCCTGGAGAAGAGTCTCGCCTCTCTACAGAAGGCCTGCCGGAAATCCAC 1328	TCGGGAACCGCTTGGAAAGGTGTCTCTCTCTCTCTCTGAAAGGCTGCCGAAATCCAC 107	1119 CACCTTCGTATGAAACGGCTAGAATTCCTCCAGGCTAACAAAGGGCAAGAGTTACCCACC 1388 	CCTGACCAAGATAATGGCTATCATAGCCTGGAGGAGGAACATAACCTTCTCCGGATGGC	1138 CCTGACCAAGATAATGGCTATCATAGCCTGGAGGAACATAACCTTCTCCGGATGGAC 1197 1449 CCACAACATTGCACAGATAACCCAGCACAGGGGGTGTCCCTGCTGCAGACAGA	1198 CCACAACATTGCACAGATAACCCAGCACAGCGGTGTCCCCTGCTGCTGCAGACAGGCCGGAG 1257	CCACTGAGAAAAACCAGAATTGGTGATTCAAGAAGTTTCACAGAGGCCCCCAGGGAAGC

Gaps

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CATTAAAGAGTCTGG----TTTAGTGCCGTGGGAATGGGCTAGTTTAGAAGCTATGTTTG 4829
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                              Length 966
                                                                                                                            Score 810; DB 5; L
Pred. No. 8.3e-192;
0; Mismatches 25;
                                                                                                                              14.8%;
larity 96.4%;
Conservative
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
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    ACTCCAGAGTGCATTAAAGAGTCTGGTTTAGTGCCGTGGGAATGGGCTAGTTTAGAAGCT
                                 TCTTTTAAACCGGACTGCAGCTTAACAACATGATTTCAGATGATTTAGGTTTTTGTTTC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13897 row: d column: 06
High quality sequence stop: 613.
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/mol_type="mRNA"
strain=FyB\n"
/db xref="taxon:10090"
/clone="IMAGE:6398165"
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AUTHORS
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CF583619
AGENCOURT_8845828_updated NIH_MGC_137 Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                     194 CCCTC-GTGTTGATGATGTCACTCCACACAGGGTTAGTAAGAGTGCACGACAGAAAC
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                                                                                                                                           Gaps
/dev_stage="adult"
/clone_lib="Mus musculus pancreas C57BL/6J adult"
                                                                                                                                             ä
                                                                                             Length 997;
                                                                                                                                        Indels
                                                                                        Score 808.6; DB 1;
Pred. No. 1.9e-191;
0; Mismatches 30;
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96.4%;
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Best Local Similarity 96.4*
Matches 834; Conservative
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (Dasses 1 to 997)
Brakawa, T.; Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

L. Unpublished (2001)
On Jun 23, 1999 this sequence version replaced gi:5154806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-reagescriken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                      997 bp mRNA linear EST 24-OCT-2001 Mus musculus pancreas C57BL/6J adult Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant CDNA library, Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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clone 1810033K10, mRNA sequence.
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strain="C57BL/6J"
db_xref="taxon:10090"
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AV055059.2 GI:16380666
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (CE (bases 1 to 1011))

Rakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kodaa, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Sano, H., Sasaki, D., Shibata, K., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

AL Umpublished (2001)

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Garninci, P., Shibata, Y., Hayatsu, N., Sughara, Y., Shibata, Y., Hayatsu, N., Sughara, Y., Shibata, Y., Hayatsu, M., Sonno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi, K., Puliwake, S., Inoue, K., Togawa, Y., Tanaka, T., Ta
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 890)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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National Cancer Genomics

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Tissue Procurement: Geradwohl (PNAS 97 P1607-1611, 2000)
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Site 2: NotI; Library consists of a pool of clones
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mixed mouses pancreas 1 N1-MMS1, Amplified Melton mouse
islets 1 MIS1-A, and Kaestner ngn3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."
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DNA Sequencing by: Agencourt Bioscience Coxporation
Clone distribution: MGC clone distribution information can library Library in MGC. E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBDs row: h column: 10
High quality sequence stop: 675.
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  IMAGE: 6431877 3', mRNA sequence.
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/db_xref="taxon:10090"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 913)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Onpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute

Coffice of Cancer Genard Gradwoll (PNAS 97 P1607-1611, 2000)

CDNA Library Preparation: Catherine Lee, Endocrine Pancreas

Consortium
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/note="Organ: pancreas; Vector: pSPORT1; Site_1: Sal1;
Site_2: Not1; Library consists of a pool of clones
  780 TGTGTACAGTCNTTTAGGGTTACAGCACAAAAGAGA---GACCTCTGAGTCGGCGGTGGG
                                                                                  1324 GTCAATATCCAGGTTTGTTGTTCTTACCTTATGTAGAGAAAGCAAAGCAGAAAGGGCA
                                                                                                                                                                                       1384 GATAGAGCAGCCAGAAAGTGCTAGT--GTCCCCCCAAAGCGTGCTTCTAGATAGTGTGT
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can letter.//image.llnl.gov
Lttp://image.llnl.gov
Hitp://image.llnl.gov
High quality sequence stop: 672.
Location/Qualifiers
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:6431877"
/lab_host="DH10B"
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Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/dev stage="10 day old"
/clone_lib="RIKEN full-length enriched, 10 day old male
pancreas"
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/mol type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="1810033K10"
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rearrayed from the following libraries: Melton normalized mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse slelts 1 MIS1-A, and Kaestner ngn3 wt. Clones rearrayed in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."
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CA978373 946 bp mRNA linear EST 06-JAN-2003 AGENCOURT 11277002 NIH MGC 164 Mus musculus cDNA clone IMAGE:30144607 5', mRNA sequence.

RESULT 10 CA978373 LOCUS DEFINITION

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/note=wbryonic limb, maxilla and mandible, day 10.5 and
11.5; (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: 01:go-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'GACTAGTTCTAGATCCCGAGCCGCCC(T) 3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 946)

IH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLML at:
http://image.llnl.gov
Place: NDAM0057 row: f column: 08
High quality sequence start: 24
High quality sequence stop: 693.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                       (house mouse)
  GI:27511027
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                                       Mus musculus
Mus musculus
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CA978373.1
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VERSION
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QSGSLPETPBHSSGEDDWESSADBAESLKLWNSFCNSDDPYNPLNFKAPFGTSGEN
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YTFLEBVTEYYISGDSDRKGPWEEFARDGCRFQKRIQETBDAIGYCLTFEHRERMFNR
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DH10B; sites NotI + SalI"
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HOMO BapienB mRNA; CDNA DKFZp6661186 (from clone DKFZp6661186).
AL833746
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                                                                                                                                                                                                                                                             CTTTGAAAGATCCTCCTGTCCTCTTGTTTGGCTTGCACATGGCATGTGCCATACATCCAG 3854
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                                                           TCTCCCTCTTTTTTTTTTTCCCCCAGAGCTGAGGACCAAACCCAGGGCTTTGCACTTGC 482
                                                                                                                                      GAAAGTTTCTGTGTGGGAAATTTCAGTTGAAAGTTGGCTCTCTGTAGCTTTTAAGAAA 901
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKF25)s661186) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomicoschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cg1-bin/products/cl.cgi?cloneID=DKFZp6661186
Further information about the clone and the sequencing project is
available at http://mps.gsf.de/projects/cdna/.
Location/Qualifiers
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1 (bases 1 to 3941)

Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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/mol type="mRNA"
/db_xref="RZPD:DKFZp6651186"
/db_xref="taxon:9606"
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Tissue Procurement: Dr. James Lin University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

were found in this cDNA

The following repetitive elements were found in this sequence: 602-707, >B1-F#SINE/Alu (matched compliment)

Seq primer: pYX-5.
Location/Qualifiers

/organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6"

tissue_type="whole eye" /db xref="taxon:10090" /clone="IMAGE:30686164"

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennidjanusen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiaMila23 row: a column: 23
High quality sequence stop: 785.
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  AGAGTTTCCCTTAAAAACAAACACTGGCAGCTGTCCTTGGACATGTTTTTAAAGAAACAA 480
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                             CTTGTATCTAGAGATGCAGTTTGATTATTTTTGGGTAATGTGTCTCATTAGAAACACCAA
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UI-WHEG-Cmb-g-24-0-UI.rl NIH_BMAP_HEG MUS musculus cDNA clone IMAGE:30627143 5', mRNA sequence.
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Score 767.4; DB 4;
Pred. No. 4.1e-181;
0; Mismatches 6;
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  14.0%;
ilarity 99.1%;
Conservative
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601

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CF617044 B35 bp mRNA linear EST 01-OCT-2003
AGENCOURT 15763558 NIH MGC_204 Mus musculus cDNA clone
IMAGE:30527269 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         1511 CACTGAGAAAAACCAGAATTGGTGATTCAAGAAGTTTCACAGAGCCCCCAGGGAAGCAG 1570
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                                                                                          gecaacceccregagaagargrececcrereracagaaggecrecegaaarecaca
                                                                                                                                  1331 CCTTCGTATGAAACGGCTAGAATTCCTCCAGGCTAACAAAGGGGCAAGAGTTACCCCCCC
                                                                                                                                                                      482 ccricciargaaacgccragaariccrccaggcraacaaaggcaagagriacccaccc
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Site_2: Not I: The library was constructed according
Site_2: Not I: The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.Pirst strand cDNA synthesis was primed with Oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with Not! and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 854)

1 MIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

1 Contact: Robert Strausberg, Ph.D.

1 Email: cgapbs-r@mail.nih.gov

1 Tissue Procurement: Dr. James Lin Unive

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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/note="Organ: placenta; Vector: pExpress-1; Site_1: ECORV; Site_2: Not1; RNA obtained from three placentas from female C57/BLG mouse at 16 days pregnancy. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primer: 5'-pGACTAGTTCTAGATCGGAGCGCCCC(T) 25-3' and cloned into the ECORV/NOTS sites of pExpress-1. Size-selection >0.75kb resulted in an average insert size of 1.1 kb. This primer; nanoquantity library is normalized to COC5 (non-normalized primary library is normalized to COC5 (constructed by Express Genomics (Frederick, MD)."
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                LPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYLDYLPQLGLRCQSSAGGG
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detection; diagnosis; antisense therapy; gene therapy

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Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                               Human protein sequence SEQ ID NO:18965
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                                                                                              Human; primer;
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                                                             The present invention relates to a method of screening several test substances for preventing or treating diseases involving oxidative stress such as neuronal ischaemia, heart ischaemia, renal damage induced by ischaemia or toxins, autoimmune diseases and neurodegenerative disorders. The method involves testing the test substances for its ability to inhibit the activity of GADD34-1ike (GADD34L), also referred to as elf2alpha specific regulatory subunit of phosphatase, and identifying the test substance which inhibits the activity of GADD34L. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDDWEPSADEAENLKLWNSPCHSEDPYNLLNPKAPPQPSGKNWKGRQDSKASSEVTVAPS 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 GHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRK 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYTSGDEDRK 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSAGGGQFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRMR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTEKKPELVIQEV----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWN 464
                                                                                                                                                                                                                                                                                                                                                        1 MEPGTGGSRKRLGPRAGFRFWPPPFRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV 60
                                                                                                                                                                                                                                                                                                                                      1 METGTHRARKRPGPRLGSWFRLPFL-RRSHACSSEFPPPSSRQNPGN----SALPERRT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSGSCGV-GSCQEGPLPETPDHSSGE
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                  Length 713;
                                                                                                                                                                                                                                                                  59.9%; Score 2223; DB 8; Length 7 65.0%; Pred. No. 5.6e-190; ive 53; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 700
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                               Disclosure; SEQ ID NO 2; 30pp; English
                                                                                                                                                                                                  sequence is the human GADD34L protein
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                    Sequence 713 AA;
                                                                                                                                                                                                                                                                                                     456;
GADD34L
                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 456
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Yamamoto

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Saito K, , Otsuki

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Hayashi K, A, Nagai K

Wakamatbu

Sugiyama T,

99JP-00300253. 2000JP-00118776. 2000JP-00183767.

2000JP-00241899

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The present invention describes primer sets for synthesising 5602 full-

(a) an oligo-dr primer and an oligoniclectide complementary to the

complementary strand of a polynucleotide comprises one of the 5602

(c) an oligo-dr primer and an oligoniclestide comprises one of the 5602

(c) an oligoniclectide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination

of an oligonucleotide comprises a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a folial sequence, where the

complementary strand of a polynucleotide of sequence complementary to a

polynucleotide which comprises at least 15 nucleotides and the combination of

the 5'-end sequence(3'-end sequence is selected from those defined in the

specification. The primer sets can be used in antisense therapy and in

complementary full-length cDNAs. The primers are also useful for the

detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

contains and and sequences, and AAH13632 to AAH13632 represent human amino acid sequences, and AAH13632 represent

coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYWTKLLSQLLALLPSLFQKLLLWSQLSGGLIPTRWLDFAASYSALRASRGREESDAPTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEPGIGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPILLSSAQPETRV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 METGTHRARKRPGPRLGSWFRLPFL-RRSHACSSEFPPPSSRQNPGN----SALPERRT
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Claim 8; SEQ ID NO 18965; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 713;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.6%; Score 2213; DB 4;
64.8%; Pred. No. 4.4e-189;
iive 55; Mismatches 174;
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Best Local Similarity 64.8
Matches 454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
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AAB95876 standard, protein, 713 AA

AAB95876 ID AAB9 XX

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                                                                                                                                   300 RLEFLQQASKGQDLPTPDQDNGYHSLEBEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQB
                                                                                                                                                                                                                                                        420 ACSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWN
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OKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAPTFLLEQQ
                             QKSLSSLQLD-SSDPSVTSPLDWLEEGIHWQYSPPDLXLELKAKGSALDPAAQAFLLEQQ
                                                          LWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYLDYLPQLGLRCQ
                                                                          SSAGGGOFVGFRILIPESCYLSEDGCHPOPLRAEMSATAWRRCPPLSTEGLPEIHHRRMR
                                                                                                                                                                             WLVFL-QPNQGQDLPTLDQDNGYHSLEEFHNLLRMDPQHCTDNPAQAVSPAADRP----E
                                                                                                                                                                                                                                       PTEKKPELVIOBY----SOSPOGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP
                                                                                                                                                                                                                                                                                                VCSNKLIDY ILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWN
                                                                                                                                                                                                                                                                                                                                                           SFHSVDPYKPONFTATIOTAARIAPRDPSDSGTSWSGSCGV-GSCOEGPLPETPDHSSGE
                                                                                                                                                                                                                                                                                                                                                                            SFCSVDPYNPQNFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                      EDDWEPSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                      EDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPPQTSGENEKGCRDSKTPSESIVAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective, vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein sequence SEQ ID NO:941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         684
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, culnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The colon disorders such as colon cancer. The colonnelectides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFILEQQLWGVELLPSSLQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRLYSNRELGSSPSGLLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLTPESCYLSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRMRWLVFL-QPNQGQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP----EPTEKKPELVIQE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 LLPSLFQKLLLWSQLSGGLIPTRWLDFAASYSALRASRGREESDAPTVQKSLSYTAAGLF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                 colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAPTFLLEQQLWGVELLPSSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 707;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
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54; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.2%; Score 2157.5; 64.2%; Pred. No. 4.3e
                                                                                                                              Claim 11; Page 1503-1506; 2104pp; English
                                                                                           disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.2%
Best Local Similarity 64.2%
Matches 442; Conservative
2000-587534/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 707 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; cantianemic; antianemic;
antibacterial; endocrine; cardiant; cantianemic; ancimation;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiathmatic; osteopathic; cytostatic;
neuroprotective; antidepressant; nootropic; antidaktinsonian; infection;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
wenetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopania; osteoporosis; severe combined immunodeficiency;
whistopania; osteoporosis; severe combined immunodeficiency;
whistopania; osteoporosis; severe combined immunodeficiency;
whistopania; osteoporosis;
whistopania;
whistopania
606 LGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCR 665
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                                                                FOKRIOETEVALGYCLAPEHREKMFNRLR 684
                                                                                                 treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:963.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 DPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCG 607
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anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhintits, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 QRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKGIQETEDAI
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                                                                                                                                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
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Pred. No. 1.9e-40;
8; Mismatches 24
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76.6%;
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                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                      Sequence 153 AA;
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                                                                                                                                                                                                                                                          ----AKTVTGADQ
                                                                                                                                                                                                                                                                                                                                        56 IEAAALLTPTPVSGNL-LPHGETEESGSP-----EQSQAAQRLCLVEAESSPP---
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uutics for ischaemic diseases. ABI99913 and ABI99914 represent 5 for a mouse ischaemic condition related sequence, which are u exemplification of the present invention
                                                                                                                                                                         Gaps
                                                                                                                                                                       168;
                                                                                                                                Length 657;
                                                                                                                           Query Match 5.5%; Score 204; DB 5; Length 65;
Best Local Similarity 21.5%; Pred. No. 1.2e-08;
Matches 149; Conservative 86; Mismatches 290; Indels
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      therapeutics for
                                                                                      Sequence 657 AA;
                            primers for
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The invention relates to an inducible progression-elevated gene-3 (PEG-3 gene) regulatory region functionally linked to a gene encoding a product that causes or may be induced to cause the death or inhibition of cancer cell growth. A vector of the invention which contains a gene encoding thymidine kinase or a product which causes the cell to express a specific antigen can be administered along with gancyclovir or acyclovir, or an antibody or fragment to the antigen, respectively, to treat cancer in a subject. The PEG-3 gene is useful for generating new cloning and expression vectors, transfected cells, and for developing methods for cultured growth of such cells. The PEG-3 polynucleotide is also useful as a source of primers and probes to study the progression of cancer, and to detect the presence of the gene. The present sequence represents the amino acid sequence of the rat MyD116 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHRAGOGHPCRNAEAEEGGPETTF--VCTGNAFLKAWVYRPGEDTEEDNSDSDSAEEDT 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 YTAAGLFAKTRVVSTLALARG----GTPVAVLVLRLEVKLKAQERAL---DSAAPTFLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAY------PTSQLEGGPAEN------EEDGETVKTYQASAASIAPGYKPS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 5.4%; Score 201; DB 2; Length 65
Local Similarity 21.5%; Pred. No. 2.3e-08;
1e8 149; Conservative 85; Mismatches 291; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 3A-B; 251pp; English.
                                                                                                                                                                                                                                                                                            COLUMBIA NEW YORK.
                                                                                                                                                                                                                    98US-00052753.
                                                                                                                                            99WO-US007199
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                                                                                                                                                                                                                                                                                     (UYCO ) UNIV
WO9949898-A1
                                                                                                                                                31-MAR-1999;
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                                                                        07-0CT-1999
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101 SSSLPEAWGLLDDDDGMYGEREATSVPRGQGSQFADGQRAPLSPSLLIRTLQ 224DYLPQLGLRCQSSAGGGFVGFRTLTPESCYLSEDGCHPQPLRAEMSATA	Qy 274WRRCPPLSTEGLPEIHHRRWRWLVFLQPNGGQDLPTLDQDNGYHSLE 320 211 LSPGSKPSTWVSCPGEEENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE 270	Qy 321 EEHNLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLPCELPVEKE 380	QY 381 CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD 440	Qy 441 GFDSDGSLSESDVEQDSEGLHLWNSPHSVDPYKPQNPTATIQTAARIAPRDPS 493	DD 365 GSDEBEGRAESSTPATGVFLKSWVYQPGEDTEEEEDEDSDTGSAEDEREAE 417	QY 494 DSGTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWEPSADEAENLKLWNSFCHSE 547	Db 418 TSASTPPASAFLKAWYRPGEDTEEEEDEDVDSEDKEDDSEAALGEAES 466	QY 548 DPYNLINFKAPFQPSGKWWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603	Db 467 DPHEAAED 498	Qy 604 PGCGLGEATAGERYTHIKRK 623	Db 499WGEAEPCPFRVALYVPGEKFPPPWAPPRLPLRLQRRLKRPETPTHDPDFETPLKAR 554	Qy 624 KVTFLEEVTEYISGDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678	Db 555 KVRFSEKVTVHFLAVWAGPAQAARQGPWEQLARDRSRFARRITQAQEELSPCLTPAARAR 614	Qy 679 MENRLR 684	Db 615 AWARLR 620	RESULT 9	AAYB4366 ID AAYB4366 standard, protein; 674 AA. XX	AAY84366;	DT 12-JUL-2000 (first entry) XX	KW Human, apoptosis associated protein, GADD34, antiviral agent, KW growth arrest and DNA damage-inducible gene 34; viral infection; KW serine/threonine phosphatase.	AA OS Homo sapiens.	AA GB2342716-A. XX	AA PD 19-APR-2000.	AA PF 27-JUL-1999; 99GB-00017631. XX	PR 14-SEP-1998; 98GB-00020025. XX			DR WPI; 2000-285397/25. DR N-PSDB; AAZ99766.
: : :	5 8 5	652 DGCRPQKRIQETEVAIGYCLAFEHREKMFNRLR 684	8 July	AAW99891 ID AAW99891 Btandard; protein; 674 AA.	AA AAW99891;	DT 09-JUN-1999 (first entry) XX	DE Human growth regulator protein GRREG.	KW Human; growth regulator protein; GRREG; cancer. XX	OS Homo sapiens.	AA WO9902680-A1.	AA PD 21-JAN-1999.	AA PF 30-JUN-1998; 98WO-US013409.	AA PR 11-JUL-1997; 97US-00893852.	AA (INCY-) INCYTE PHARM INC.	PI Bandman O, Lal P, Shah P, Corley NC;	XX	XX XX Novel human growth regulator protein - useful in the treatment of PT cancers.	XX PS Claim 1, Fig 1, 70pp; English.		CC GRREG. A fragment from the nucleic acid sequence encoding GRREG can be CC used as a probe for detecting GRREG encoding sequences (especially in PCR CC amplified samples)	SQ Sequence 674 AA;	Query Match 5.2%; Score 191.5; DB 2; Length 674;	bocar Similarity Zi.3%; Figures 156; Conservative 75; Mis	Qy 60 LLSQLLALLPSLPQKLLLWSQLSGCLIPTR-WLDPAASYSALRASRGREESDAPTVQKSL 118	Db 21 LLSPVMSLLSRAWSRLR-GLGPLEPWLVEAVKGAAL55	119 SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAFT	56VEAGLEGEARTPLAIPHTPWGRRPEEEAEDSGGPGEDRETLGLKT	Qy 169 FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL 223 123

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Screening assay for potential antiviral agents that modify
PT serine/threonine phosphatase activity for treating human viral
PT infections.

XX
XX
Claim 6; Page 99; 106pp; English.

XX
Claim 6; Page 99; 106pp; English.

XX
The present sequence represents a human apoptosis associated protein
CC (3ADD34). It is encoded by a growth arrest and DNA damage-inducible gene
CC 34. It is used in an assay method for identifying an anti-viral agent
CC that can affect the activity or expression of a nucleotide sequence or
CC its expression product. The assay method comprises contacting an agent
CC its expression product. And determining whether the agent affects the
CC with a nucleotide sequence coding for a serine/threonine phosphatase or
CC its expression of the nucleotide sequence. The assay is used for
CC activity or expression of the nucleotide sequence. The assay is used for
CC activity or entiviral agents useful in the treatment of human viral
CC activity inhibit the action of a host component which interferes with the
CC activity inhibit the action of a host component which interferes with the
CC activation of a host-cell interferon-induced, double-stranded RNA-
CC activation of a host-cell interferon-induced, double-stranded RNA-
CC activated protein kinase e.g. P68, eIF2 or eIF2alpha
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LISQLIALIPSIFQKILLWSQLSGGLIPTR-WIDFAASYSALRASRGREESDAPTVQKSL 118 --VEAGLEGEAR-----TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100 169 FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL---- 223 101 SSSLPEAWG--LLDD--DDGMYGEREATSVPRGQGSQFADGQ----RAPLSPSLLIRTLQ 152 --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA--- 273 -----WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE 320 211 LSPGSKPSTWVSCPGEEENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE 270 EEHNLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE 380 381 CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD 440 DSGTSWSGSCGVGSCQEGPLPETPDH----SSGEEDDWEPSADEAENLKLWNSFCHSE 547 418 TSASTPPASAFLKAWVYRPGEDTEEEEDEDVDSEDKEDDSEAALGEAES------ 466 DPYNLLNFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603 604 PGCGLGEA-----YTHIKRK 623 KVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678 KE-----BKAHKETGKGEAA-----PGPQSSAP-----AQRPQLKSWWCQPSDEEE 311 312 GEVKALGAAEKDGEAECPPCIPPPSAFLKAWVÝWPG---EDTEEEEDEEE----DEDSDS 364 GFDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ-----TAARIAPRDPS 493 365 GSDEEEGEAEASSSTPATGVFLKSW------VYQPGEDTEEEEDEDSDTGSAEDEREAE 417 ----WGRAEPCPFRVAIYVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHDPDPETPLKAR 554 SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T Gaps Query Match 5.1%; Score 189.5; DB 3; Length 674; Best Local Similarity 21.5%; Pred. No. 2.6e-07; Matches 156; Conservative 74; Mismatches 269; Indels 227; DPH-----PSHPDQRAHFRGWGYRPGKETEEE--Best Local Similarity 21.5 Matches 156; Conservative 9 21 119 26 224 274 321 494 548 467 624 271 499 441

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a arrangle trasue of a first animal that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compound that regulates the activity of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating computed by sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the specification, but was obtained in electronic form darring an electronic form darring to method. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form darring parent of the specification, but was obtained in electronic form darring patent of the proposition of the profile of t
555 KVRFSEKVTVHFLAVWAGPAQAARQGPWEQLARDRSRFARRITQAQEELSPCLTPAARAR 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                           ADE54748 standard; protein; 674 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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                               WO2003016475-A2.
          Homo sapiens.
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                                                                           60 LLSQLLALLPSLFQKLLLWSQLSGGLIPTR-WLDFAASYSALRASRGREESDAPTVQKSL 118
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                                                                                                                                                                                                                  --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA--- 273
                                                                                                                                                                                                                                                                                                                                                                                GEVKALGAAEKDGEAECPPCIPPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                      227;
                                DB 7; Length 674;
                               5.1%; Score 189.5; DB 7; Length 6
21.5%; Pred. No. 2.6e-07;
ive 74; Mismatches 269; Indels
                                                                                                 LLSPVMGLLSR-----AWSRLR-GLGPLEPWLVEAVKGAAL
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                                          Best Local Similarity 21.5
Matches 156; Conservative
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The invention discloses a composition comprising two or more isolated rate or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynuclectides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a compound or activity in an animal of one or more of the polypeptides given in the production of a pharmaceutical composition, a method for identifying a compound expect in the cativity in an animal of now or more of the polypeptides given in the production and animal of now or more of the polypeptides given in the production and paramaceutical composition or an endicating and animal or now or identifying a compound useful in the production and animal compound use of the polypeptides given in the production and animal compound use of the polypeptides given in the production and animal compound use of the polypeptides given in the production of the polypeptides given in the production of the polypeptides given in the production of the polypeptides of the polypeptides given in the production of the polypeptides of the polypeptides given in the production of the polypeptides of the polypeptides given in the production of the polypeptides of the polypeptides given in the production of the polypeptides 
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                       Claim 1; Page; 1017pp; English.
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GEBKAEEEGVAEEEGVIKFSYPPSHRECCPAVEEEDDEKAVKKEAHRTSTSA 210
                                                                                           -----WRRCP----PLSTEGLPEIHHRRMRWIVFLQPNQGQDLPTLDQDNGYHSLE 320
                                                                                                                                                                                                                      REHNLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 GEVKALGAAEKDGEAECPPCIPPPSAPLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 GSDEEEGEAEASSSTPATGVFLKSW------VYQPGEDTEEEEDEDSDTGSAEDEREAE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSGTSWSGSCGVGSCORGPLPETPDH----SSGEEDDWEPSADEAENLKLWNSFCHSE 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPYNLLNFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603
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                                                                                                                                                        211 LSPGSKPSTWVSCPGEBENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE
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htal nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE54744 standard; protein; 674 AA
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spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the apparanceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that molates its activity is useful for preparing a medicamental pares in any of a polymental narve infury. (Phumo) chronic constriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                         New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                      Claim 1; Page; 1017pp; English.
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Sequence 674 AA;

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                                                                                                                                                                                                                                                                                                                                                                                               SSSLPEAWG--LLDD--DDGMYGEREATSVPRGQGSQFADGQ----RAPLSPSLLIRTLQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEDKNP--GEEKAEEEGVAEEEGVNKFSYPPSHRECCPAVEEBDDEEAVKKEAHRTSTSA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GEVKALGAAEKDGEAECPPCIPPPSAFLKAWVYWPG---BDTEEEEDEEE----DEDSDS 364
                                                                                                             LLSQLLALLPSLFQXLLLWSQLSGGLIPTR-WLDFAASYSALRASRGREESDAPTVQKSL 118
                                                                                                                                                                                                                                                                               --VEAGLEGEAR-----TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ----TAARIAPRDPS 493
                                                                                                                                                                                                                                                                                                                                          FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA---
                                                                                                                                                                                                                          119 SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T
                                                        227;
  Length 674;
                                                                                                                                                                     LLSPVMGLLSR-----AWSRLR-GLGPLEPWLVEAVKGAAL-----
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5.1%; Score 189.5; DB 7;
21.5%; Pred. No. 2.6e-07;
tive 74; Mismatches 269;
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                          Best Local Similarity
Matches 156; Conserv
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     Query Match
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DSGTSWSGSCGVGSCQEGPLPETPDH----SSGEEDDWEPSADEAENLKLWNSFCHSE 547

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ADR14089 standard; protein; 674 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in
                                                                                                   DPYNLLNFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603
                                                          ------EAAED-- 498
                                                                                --YTHIKRK 623
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                                                                                                                                            full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
| :: | : | | : | TSASTPPASAFLKAWYRPGEDTBEEDEDVDSEDKEDDSEAALGEAES------
                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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Wakamatsu A, Nagai K,
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11-JAM-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-UDM-2000; 2000JP-00241899.
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gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or disgnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSPVMGLLSR-----AWSRLR-GLGPLEPWLVEAVKGAAL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VEAGLEGEAR-----TPLA--IPHTPWGRRPGEEAEDSGGPGEDRETLGLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 LSPGSKPSTWVSCPGEEENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 KE-----BKAHEETGKGEAA-----PGPQSSAP-----AQRPQLKSWWCQPSDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ-----TAARIAPRDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSGTSWSGSCGVGSCQEGPLPETPDH-----SSGEEDDWEPSADEAENLKLWNSPCHSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 TSASTPPASAFLKAWVYRPGEDTEEEEDEDVDSEDKEDDSEAALGEAES------
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                                                                                                                                                                                                                                                                                                                                                                                   227;
                                                                                                                                                                                                                                                                                                                              Length 674;
                                                                                                                                                                                                                                                                                                                                                                                   IndelB
                                                                                                                                                                                                                                                                                                                        Query Match 5.0%; Score 186.5; DB 4; Best Local Similarity 21.5%; Pred. No. 4.9e-07; Matches 156; Conservative 73; Mismatches 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 PGCGLGEA-----LAGER----
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                                                                                                                                                                                                                       present invention
                                                                                                                                                                                                                                                                               Sequence 674 AA;
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The introductor relates to the novel association of protein squares (and the genes which encode them) to the NF-kapaB pathway. The invention may be useful for the production of compounds with an antinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiasthmatic, antiarthritic, antirheumatic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or culmerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kapaB pathway. The condition is an immune disorder, an inflammatory disorder.

CC diseases associated with the NF-kapaB pathway. The condition is an condition of disease. Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, immunodeficiency, viral infections, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell cetodermal dysplasia, steuman activity, disorders athema, atherosclearosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant conditions, conditions related to organ transplant crejection, conditions related to organ transplant crejection, conditions and the path of a human protein which is subject to the novel association with the NF-kapaB pathway of the NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hyper-Igh syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral infection; how call survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; attenceclerosis; cachexia; euchyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; (and New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway. aberrant acute phase response; hypercongenital condition; birth defect, necrotic lesion; wound, organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; This invention relates to the novel association of protein sequences Human NF-kappaB pathway-associated protein SeqID90, Carman J; Claim 6; SEQ ID NO 90; 237pp; English. Feder JN, (BRIM) BRISTOL-MYERS SQUIBB CO. 14-JAN-2003; 2003US-0440068P. 12-MAY-2003; 2003US-0469757P. 13-JAN-2004; 2004WO-US000798 (first entry) Nadler SG, Neubauer MG, HIV propagation; human 2004-562168/54. N-PSDB; ADR14088. WO2004065577-A2 Homo sapiens 21-OCT-2004 05-AUG-2004 ADR14089;

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32;
                                                                                                                                                               60 LLSQLLALLPSLFQKLLLWSQLSGGLIPTR-WLDFAASYSALRASRGREESDAPTVQKSL 118
                                                                                                                                                                                                                                                                      --VEAGLEGEAR-----TPLA--IPHTPWGRRPGEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                               SSSLPEAWG--LLDD--DDGMYGEREATSVPRGQGSQFADGQ----RAPLSPSLLIRTLQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 LSPGSKPSTWVSCPGEBENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                     SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T 168
                                                                                                                                                                                                                                                                                                                                                                             --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA--- 273
                                                                                                                                                                                                                                                                                                                                                                                                          GSDKNP--GEEKAEEEGVAEEEGVNKFSYPPSHRECCPAVEEEDDEEAVKKEAHRTSTSA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 KE-----EKAHEETGKGEAA-----PGPQSSAP-----AQRPQLKSWWCQPSDEEE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 SEVKPLGAAEKDGEAECPPCIPPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----WGEAEPCPFRVAIYVPGEKPPPWAPPRLPLRLORRLKRPETPTHDPDPETPLKAR 554
                                                                                                                                                                                                  25
invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.
                                                                                                                                                                                                LLSPVMGLLSR-----AWSRLR-GLGPLEPWLVEAVKGAAL-------
                                                                                                                                                                                                                                                                                                         FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEHNLLRMDPOHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE
                                                                                                                              Gaps
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                                                                                                                            Indels 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Progression elevated gene-3; PEG-3; human; tumour progression;
                                                                                         Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human progression elevated gene-2 (PEG-3) protein.
                                                                                        DB 8;
                                                                                                                         73; Mismatches 270;
                                                                                        5.0%; Score 186.5; DB
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                                                                                                            21.5%;
                                                                                                                         Matches 156; Conservative
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                                                                                                            Similarity
                                                        Sequence 674 AA;
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                                                                                         Query Match
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New isolated Progression Blevated Gene-3 - used to develop products for e.g. modulating DNA damage and repair pathways, cancer progression or oncogene mediated transformation and angiogenesis.
DNA replar; tumorigenesis; angiogenesis; metastasis; melanoma;
brain cancer; cervix cancer; prostate cancer; lung cancer;
colorectal cancer; neuroblastoma; glioblastoma; diagnosis; therapy.
                                                                                                                                              Zhang N;
                                                                                                                                             Su Z,
                                                                                                                   (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                   97US-00821818.
                                                                                   98WO-US005793
                                                                                                                                             Pisher PB, Goldstein NI,
                                                                                                                            (GENQ-) GENQUEST INC
                                                                                                                                                             WPI; 1998-557025/47.
N-PSDB; AAV65765.
                                                                                   20-MAR-1998;
                                                                                                    21-MAR-1997;
                                  Homo sapiens
                                                 WO9842315-A1
                                                                  01-OCT-1998
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Claim 17; Fig 13A-C; 225pp; English.

This polypeptide comprises human progression elevated gene-3 (PEG-3) protein. The amino acid sequence was deduced from an isolated CDNA clone (see AAV65765). PEG-3 expression (1.5 and 2.8 kb transcripts) is elevated in most human tumour cell lines. The amount of PEG-3 in a cell is also an indicator of DNA damage in that cell. Cells in which a reporter gene in under control of the promoter or regulatory region (see AAV65766) of the rat PEG-3 gene can be used in methods for identifying agents that modulate PEE-3 expression or the ability of PEG-3 to induce progression, or for determining whether an agent is capable of inhibiting DNA damage and repair pathways, cancer progression or oncogene-mediated rannals and repair pathways, cancer progression or oncogene-mediated can any agent is an also be identified using send cells. Transgenic animals and vaccines comprising PEG-3 pulpapetides and an immune response channed to claimed. Antibodies (especially monoclonal) to the PEG-3 may be used to determine tumour progression of a cell. Cells can be protected from chemotherapeutic damage by inhibiting or eliminating the expression of PEG-3 in the cells. The methods can be applied to a protected from chemotherapeutic admage by inhibiting or eliminating the tumour grognession and applied to a protected stands or managemage or managemagemagemagemic tumorigenesis, and agglessis or metastesis, to melanoma, brain, cervical, tumorigenesis, lung or colorectal cancer, neuroblastoma or glioblastoma (all

Sequence 578 AA;

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216 YLLNPSYLDYLPQLGLR------CQSSAGGGQFVGFRTLTPESCYLSEDGCHPQP 264
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                                                                                                                                                                                                                                                                                                                                                                                          296 LVFLQP--NQGQD-------LPTLDQDNGYHSLEEEHNLLRMDPQHCTDN 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 LSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSPLMGLLSR-----AWSRLRGPEVPRAWL-------AKTVTGADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 204; DB 3; Length 657; Best Local Similarity 21.5%; Pred. No. 9.4e-10; Matches 149; Conservative 86; Mismatches 290; Indels 168; Gaps
                                                                                                                            GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,852A
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ALIGNMENTS
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                                                                                      Sequence 3, Application US/08893852A Patent No. 6080558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 657 amino acids amino acid
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MEDIUM TYPE: Diskette
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TOPOLOGY: line:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                               STATE: CA
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US-08-893-852A-3
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200 TPVPFIGEAEHQATE----EKGTENKADPSNSPSSGSHSRAWEY-YSREKPKQEGEAKVE 254
                                                                                                                                                                                                                                   313 AQTGATPHTSAFLKAWVYRPGEDTEEEDSDSDSAREDTAQTGATPHTSAFLKAWVYRPGE 372
                                                                                  340 AVSPAADRP----EPTEKKPELVIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRG 395
                                                                                                                       436 EPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDS 495
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                                                                                                                                                                                                                                                                                                                                                                373 DTEEENSDLDS--AEEDTAQTGATPHT-SAFLKAWVYRPGEDTEEENSDLDSAEEDTAQT 429
                                                                                                                                                                                                                                                                                                                                                                                                                      496 GTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNF 555
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                                                                                                                                                                                                 396 ESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESED------W----GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 ĠATPHTSPFLKAWVYRPGEDTEDDTEEEDSENVAPGDSFTADSSQSPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION OF THE PROGRESSION ELEVATED GENE-3 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPALIZE
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
CARTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fisher, Paul B.
TITLE OF INVENTION:
INVENTION: ELEVATED GENE-3 AND WINGER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Albert wai-Kit
REGISTRATION NUMBER: 36,479
REPRENCE/DOCKET NUMBER: 51523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/08821818; Patent No. 6146877; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 657 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
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ORGANISM: rat
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US-09-052-753B-3
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                                                                                                                                                                                   EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLG-----NFKVVSY---LLN 219
                                                                                                                                                                                                           --ETWGLSNVDEYNAKPGQDDLREKEMERTAGKATLQPAGLQGADKRLGEVVAREEGVAE 160
                                                                                                                                                                                                                                                                                                           280 LSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQ 339
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                                                                                                                      120 YTAAGLFAKTRVVSTLALARG----GTPVAVLVLRLEVKLKAQERAL---DSAAPTFLL 171
                                                                                                                                                    56 IEAAALLTPTPVSGNL-LPHGETEESGSP-----EQSQAAQRLCLVEAESSPP---- 102
                                                                                                                                                                                                                                                PSYLDYLPQLGLRCQSSAGGGQFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPP 279
                                                                                                                                                                                                                                                                           161 PAY------PTSQLEGGPAEN------EEDGETVKTYQASAASIAPGYKPS 199
                                                                                                                                                                                                                                                                                                                                      200 TPVPFLGEAEHQATE----EKGTENKADPSNSPSSGSHSRAWEY-YSREKPKQEGEAKVE 254
                                                                                                                                                                                                                                                                                                                                                                        AVSPAADRP----EPTEKKPELVIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNF 555
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                                                                                         -----AKTVTGADQ 55
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                                 Gaps
                                168;
5.5%; Score 204; DB 3; Length 657; 21.5%; Pred. No. 9.4e-10;
                              86; Mismatches 290; Indels
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APPLICANT: Paul B. Fisher
TITLE OF INVENTION: Progression Elevated Gene-3 and Uses:
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
FILE REPERENCE: A34608-B
CURRENT APPLICATION NUMBER: US/09/052,753B
CURRENT APPLICATION NUMBER: US/09/052,753B
CURRENT APPLICATION NUMBER: D6/812,818
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | :|| : | | :| : ||| DRSRFARRIAQAEEKLGPYLTPDSRARAWARLR 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGCRFQKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                                                              ||| |: ||
LLSPLMGLLSR-----AWSRLRGPEVPEAWL
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                Best Local Similarity 21.5
Matches 149; Conservative
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                                                                                                                                                                                                         120 YTAAGLFAKTRVVSTLALARG-----GTPVAVLVLRLEVKLKAQERAL---DSAAPTFLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 TPVPFLGEAEHQATE----EKGTENKADPSNSPSSGSHSRAWEY-YSREKPKQEGEAKVE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEEENSDLDS---AEEDTAQTGATPHT-SAFLKAWVYRPGEDTEBENSDLDSAEEDTAQT
                                                                                                                                                                                                                                                                                                             EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLG-----NFKVVSY---LLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEFHNLLRMDPQHCTDNPAQ
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                                                                                                                                                        ----AKTVTGADQ
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                                                   Indels 168; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESED--------
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  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 KAPFQPS----GKNWKGRQDSKASSEVTVAFSGHH-----
Query Match 5.5%; Score 204; DB 4; L
Best Local Similarity 21.5%; Pred. No. 9.4e-10;
Matches 149; Conservative 86; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN GROWTH REGULA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGCRFQKRIQETEVAIGYCLAFEHREKMFNRLR
                                                                                                                                       Sequence 1, Application US/08893852A, Patent No. 6080558, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
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-- YTHIKRK 623

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524 KUTFLEEVTEYYIS----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678
                                                                                                          LR-----TEGLPEIHHRRWRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 LRETEGNGTPEWSKAAQRLCLDVEAQSSPPKTWGLSDIDEHNGKPGQDGLREQEVEHTAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 LVFLOP--NQGQD-------LPTLDQDNGYHSLEEEHNLLRMDPQHCTDN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 LPTLÓPLHLÓGADKKVGEVVAREEGVSELAYPTSHWEGGPAEDÉEDTETVKKAHQASAAS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 PAQAVSPA-----ADRPEPTEKKPELVIQEVSQSPQGS-SLFCELPVEKECEE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 DHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDW----GEEPED 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 DGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSW 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLL 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 YLLSP-LMGFLSRAWSRLRGPEVSEAWLAETVAGANQIQADALLTPPP--VSENHL---P 73
                                              ----WGEAEPCPFRVAIYVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHDPDPETPLKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 YLLNPSYLDYLPQLGLR-----CQSSAGGGQFVGFRTLTPESCYLSEDGCHPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSCGVGSCQEGPLPET----PDHSSGEEDDWEPSAD-EAENLKLWNSFCH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%; Score 182.5; DB 4; Length 578; 22.7%; Pred. No. 7.5e-08; Live 61; Mismatches 213; Indels 169
                                                                                                                                                                                                                                                                                                                                FALCHIL NO. 94 / 220

FARENEAL INFORMATION: Progression Elevated Gene-3 and Uses;

TITLE OF INVERTION: Progression Elevated Gene-3 and Uses;

TITLE OF INVERTION: Thereof;

FILE REFERENCE: A34608-B: US/09/052,753B

CURRENT APPLICATION NUMBER: US/09/05793

FRIOR PILING DATE: 1998-03-31

FRIOR FILING DATE: 1998-03-20

FRIOR FILING DATE: 1998-03-21

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 578
                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/09052753B ; Patent No. 6472520
            --LAGER
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                                                                                                                                                               679 MFNRLR 684
                                                                                                                                                                                                     615 AWARLR 620
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130; Conserv
            504 PGCGLGEA-
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VEAGLEGEAR-----TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL---- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSLPEAWG--LLDD--DDGMYGEREATSVPRGQGSQFADGQ----RAPLSPSLLIRTLQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNGGODLPTLDQDNGYHSLE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 LSPGSKPSTWVSCPGEEENQATEDKRTERSKGARKTSVSPRSGSDPRSWEYRSGEASEE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEHNILRANDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSDEERGEAEASSSTPATGVFLKSW-----VYQPGEDTEEEEDEDSDTGSAEDEREAE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 SEVKALGAAEKDGEAECPPCIPPPSAFLKAWVÝWPG---EDTEEEEDEEE----DEDSDS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ-----TAARIAPRDPS 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSGTSWSGSCGVGSCQEGPLPETPDH----SSGEEDDWEPSADEAENLKLWNSFCHSE 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPYNLLNFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 TSASTPPASAFLKAWVYRPGEDTEEEEDEDVDSEDKEDDSEAALGEAES------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227;
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COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,852A
FILING DATE: Filed Herewith
APPLICATION DATA:
APPLICATION NUMBER: US/08/693,852A
FILING DATE: Filed Herewith
APPLICATION NUMBER: US/08/693,852A
FILING DATE: Filed Herewith
APPLICATION NUMBER: BS-08/693,852A
TYCANEY/AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: BF-0341 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-865-0556
TINFORMATION: NO. 11
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                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
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LIBRARY: TMLR3DT01
CLONE: 508302
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Matches 156; Conserve
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268 VSSLSVSSGNAFLKAWVYRPGEDTEDDDSDWGSAEEEGKALSSPTSPE----HDFLKA 322
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                                                                                                                                                                                                                                                                                                                                                                                                        417 GAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQN 476
                                                                                                                                                                          ------EDDQDSDWGSAEKDGLAQTFATPHTSAFLKTWVCCPGEDTEDDDC 416
                                                                                                                                                                                                                    517 ----PDHSSGEEDDWEPS-----ADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGK 564
                                                                                                                                                                                                                                                       417 EVVVPEDSEAADPDKSPSHEAQGCLPGEQTEGL-----VEAEHSLFQVAPYLPGEKPAP 470
                                                                                                                                                                                                                                                                                                                                                                             625 VIFLEEVIEYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEVALGYCLAFEHREKM 679
                                                                                        323 WVYRPGEDTEDDDDSDWGSAEE-----EGKALSSPTSPEHDFLKAW-----VYRPGE
                                                                                                                                                                                                                                                                                                 565 NWKGRODSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08821818
Patent No. 6146877
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: IDENTIFICATION OF THE PROGRESSION
TITLE OF INVENTION: ELEVATED GENE-3 AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCES: 5
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                      477 FTATIQTAARIAPRDPSDSGTSWSGSCGVGSCQEGPLPET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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18.1%; Pred. No. 8.1e-07;
cive 68; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 51523
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 WARLGNPSLPLAL 578
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Best Local Similarity 18.1<sup>§</sup>
Matches 100, Conservative
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MOLECULE TYPE: protein
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TEKKPELV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----STEGLPEIHHRR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- XHSLEEEH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 IQEVSQSPQGSSL--FCELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILG 416
  597 ESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYIS----GDEDRKGPWEEFAR 651
                                       -----PARNQGPEIP-----LKGRKVHFSEKVTVHFLAVWAGPAQAARRGPWEQFAR 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.6%; Score 171.5; DB 3; Length 590; 18.1%; Pred. No. 8.1e-07;
                                                                                                                                                                                                                Sequence 4, Application US/08893852A
Patent No. 6080558
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Shah, Pureti
APPLICANT: Shah, Pureti
APPLICANT: Corley, Nuril
CORNESSONDENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 NLLRMDP------QHCTDNPAQAVSPAADRPEP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 PESCYLSEDGCHPQPLRAEMSATAWRRCPPL-----
                                                                                                         | | :|| :|| | :|| | CRSRFARRIAQAEEQLGPYLTPAFRARAWTRLR 527
                                                                               652 DGCRFQKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PESESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,852A
FILIMG DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 MRWLVPLQPNQGQDLPTLDQDNG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0341 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 100; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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LIBRARY: General
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ჟ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Pal
STATE: CA
                                                                                                                                                                                                 US-08-893-852A-4
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                                          448
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Maintenance	OY 250 PESCYLSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRR 292	Db 163 SHWEGCPSEBEBGBETVKKAFRASADSPGHK
VSPANDERED:	293 MRWLVFLQPNQGQDLPTLDQDNGYHSLEEEH	324
SERIOR S	163 SHWEGCPSEEEEDGETVKKAFRASADSPGHKSSTSVYCPGEAEHQATEEKQ 324 NLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELV ::	
SECRETARE STATES AND ATTER ATT	214 TENKADPPSSPSGSHSKAMEYCSKQEGEADPEPHRAGKYQLCQNAEAEEEEEAK 359 IQEVSQSPQGSSLPCELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILG : :	417
CANADASSIPPENDILARM	268 VSSLSVSSGNAFLKAWVYRPGEDTEDDDDSDWGSAEEEGKALSSPISPEHDFLKA 417 GAPSDLEASBDSESEDWGEBPEDDGFDSDGSLSESDVBQDSEGLHLWNSFHSVDPYKPQN	477
ABULKLWNSPCHSEPKTWVCCPGEDTEDDDC 416	323 WVYRRGEDIEDDDDSDWGSAEKEGKALLSSPISPEHDFLKAWVYRPGE 477 FTATIQTAARIAPRDPSDSGTSWSGSCGVGSCQBGPLPET	517
	370 DTEDDQDSDWGSAEKDGLAQTFATPHTSAFLKTWVCCPGEDTEDDDC 517PDHSSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGK	565 NWKGRQDSKASSEVTVAFSGHHTLLSCKAQL: :: :
Oy 660 PMRIRIESKOLLL 692 566 11 11 11 11 11 12 12	417 EVVVPEDŠEAADPDKSPŠHEAQGCLPGEQTEGLVEAËHSLFQVAFYLPGEKPAP 565 NWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKK 11	625 VTPLEEVTEYYISGDEDRKGPWEEFAL
RESULT 9 Sequence 11618 Application US/09949016	4/1 FW	680 FNRLRIESKDLLL : 566 WARLGNPSLPLAL
Gene-3 and Uses Gene-14-14 Gene-14-14-15-5 FRIOR PILING DATE: 2000-10-20 FRIOR FILING DATE: 2000-10-20 GOFTWARE FARICATION NUMBER: 60/231/498 FRIOR FILING DATE: 2000-10-20 GOFTWARE FASTER OF FEINT ASSOCIATION A	680	pplication US/0994901
	Gene-3 and Uses Gene-3 and Uses 3B 5. DB 4; Length 590; 8.1e-07; 1. Length 187; Gaps PLSTEGLPEIHHRR 2	GENERAL I APPLICAN TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF TITLE OF PRIOR AP PRIOR AP PRIOR PI PRIOR PI PRIOR PI PRIOR PI PRIOR PI TYPE: P ORGANIS O'9-949-0

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ASSOCIATED OF DETECTION AND USES THEREOF
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: : ||:
HKSSTSVYCPGEAEHQATEEKQ 213
                                   P----TEKKPELV 358
                                                    GESLPVSTRPVCSNKLIDYILG 416
                                                                                                    ODSEGLHLWNSFHSVDPYKPON 476
                                                                                                                                                    HTSAFLKTWVCCPGEDTEDDDC 416
                                                                                                                                                                                                                                    FCHSEDPYNLLNFKAPFQPSGK 564
                                                                                                                                                                                                                                                        -VEAEHSLFQVAFYLPGEKPAP 470
                                                                                                                                                                                                                                                                                  ICPGCGLGBALAGERYTHIKRKK 624
                                                                                                                                                                                                                                                                                                                                  KRIQETEVAIGYCLAFEHREKM 679
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RRIAQAEEKLGPYLTPAFRARA 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLWSQLSGGLIPTRWLDFAA 95
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Qy 5 THRARKRPGPRLGSWFRLPFLRSHACSSEFPP	65 LALLPSLEQ		153	213 VVSY : :	272 272 1412	309	361	377		Db 1649 DDFSQHDQDKSPLSDSGFETRSEKTPS-APGSA Qy 485 ARIÄPRDPSDSGTSWSGSCGVGSCQEGPLPETP	Qy 545 HS-EDPYNLINFKA	, STATE: California
OY 156 KAQERALDSAAPTFILEQQLWGVELLPSSLQAGLVSHRE 194	OY 195 LDSSSSGPLSVQSLGNFKVVSYLLNPSYLDYLPQLGLRCQSSAGGQFVGFRTLTPESCY 254	OY 255 LSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRNEWLVFLQPNQGQDLPTLDQDN 314	Oy 315 GYHSLEEEHNLLRMDPQHCTDNPAQAVSPADRPEPTEKKPEL 357 	Oy 358 -VIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP- 404 1	QY 405 -VCSNKLIDYILGGAPSDLEASSDSRSEDWGEEPEDD 440 :::	OY 441 GPDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDSG 496	QY 497 TSWSGSCGVGSCQRGPLPETPDHSSGEEDDWEPSADEAENLKIWNS 542	Qy 543 FCHSEDPYNLLNFKAPPQPSGKOWKGRQDSKASSEVTVAFSGHHTLLS 590 1	OY 591 CKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEE 648 ::::	Qy 649 PARDGCRFQKRIQETEVALGYCLAFEHREKMFNRLRIESKDLLL 692 	US/09949016 US/09949016 G et al. RPHISMS IN KNOWN GENES ASSOCIATED HUMAN DISEASE, METHODS OF DETECTION AND USES TH 1 US/09/949,016 60/241,755 60/237,768 60/231,498 12 Ows Version 4.0 4%; SCOTE 127.5; DB 4; Length 3913; 14; Pred. No. 0.2;	, Conservative 11.

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| : | : : | : CRSPTFMELEPKPTTSSIKEKVKAFQMKA 1759
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PPSSRQNPGNSALPERRIRYWTKLLSQL 64
                                                                             | | | | : | ::
|SESPVKQMPGHAEVALVNGSISPLKYPS 1263
                                                                                                                                                                                         TDNPAQAVSPAADR-PEPTEKKPELVIQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                VYNLTKVIDYLTNDIGSSSLTNLKYKFED 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDTVEXVESTIT----AMPRSPL---- 1314
                                                                                                                                                                      LOAGLVSHRELDSSSSGPLSVQSLGNFK 212
                                                                                                                                                                                                                                                   SEGLHLWNSFHSVDPYKPQNFTATIQTA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDHSSGEEDDWEPSADEAENLKLWNSFC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAPFOPSGKNWKGR-QDSKASSEVTVAFS 583
                                                                                                               SLFAKTRVVSTLALARGGTPVAVLVLRLE 152
                                                                                                                                                                                                                                                                                      ITHHRRMRWLVFLQPNOGQDLP----- 308
                                                                                                                                                                                                                                                                                                                                                                                                     -----B3SLFCEL----P376
                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VSTRPVCSNKLIDYILGGAPSDLEAS 425
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                                                                                                                                                                                                                             FRILIPESCYLSEDGCHPOPLRAEMSA- 271
                                                        LIS-----GGLIPTRWLD 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REKMFNRLRIESKOLL 691
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US-09-698-295-10; Sequence 10, Application US/09698295; Patent No. 6689584; GENERAL INFORMATION:
  1373 TKELGPCG 1380
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-698-295-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1143 EQSPAAQDSCLEARKSQPDESCLSALHNSSDLELRATPEPAQT-------GVP 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1189 QQVHPTEDEASSPWSVLNAELSSGDDFETQDDRPCTLASTGTNTNELLAYTNSALDKSLS 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1329 H.----RSLLKPTAANAPD-PLPEDWKKE-----KKAVTPFDDVTVYLF----DQETP 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TPDS--LESVDVHEALLDSLGSHTPQKLVPPDKPAD 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1030 SGYETENLESPE-----WILHPAPEGTADSEPATTGDGGHSGLPPNPVIVISDAGDGH 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1249 SHSEGP----SCHLDLSEDGMDADEE 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1288 D-ENSDDSDEDLRAFNLHSLSSESEDETEHPVPIILSNED--------GR 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 LEQQLWGVELL-----PSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYLD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            940 LEKNLEAVETLNQINSKDAAKEAGLVSALSSDSTSQDSLLEDS-----LSAPFPA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 YLPQLGLRCQSSAGGGGFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPP---- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 --LSTEGL--PEIHHRRMRWLVFLQPNQGQDL-PTLDQDNGYHSLE------EEH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 NLLRMDPQ-------HCTDNPAQ-----AVSPAADRPEPTEKKPELVIQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVSOSPOGSSLFC-ELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAP 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 SDLEASSDSESEDW----GEEPEDDGFD-----SDGSLSESDVEQDSEGLHLWNS 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 FHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSGSCGVGSCQEGPLPETPDHSSGEED 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DWEPSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGH 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 HTLLSCKAQLLESQEDNCPGCGLGBALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 127; DB 3; Length 1503;
21.4%; Pred. No. 0.049;
tive 55; Mismatches 204; Indels 172;
                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: STATEM: IBM P.C. DOS 5.0
SOFTHARE: FRASESCO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION NUMBER: 60/031,675
PILING DATE: No. 6136581ember 22, 1996
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
NAME: WATDURG, RIChard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 229/182
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEPRA: (213) 555-0440
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1503 amino acid8
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.49
Best Local Similarity 21.49
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990 SEPSLE-----
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US-08-976-255-14
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JARBARAL INFORMATION: Michael H.

TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY FACTOR
FILE REFERENCE: 06501-068001

CURRENT APPLICATION NUMBER: US/09/698,295

CURRENT FILING DATE: 2000-10-27

FRIOR APPLICATION NUMBER: PCT/JP99/02340

PRIOR FILING DATE: 1999-04-30

PRIOR PILING DATE: 1999-04-30

PRIOR PILING DATE: 1999-04-30

FRIOR PILING DATE: 1998-04-30

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10

LENGTH: 2781
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Patent No. 6689584
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY FACTOR
FILE REPERENCE: 06501-068001
CURRENT APPLICATION NUMBER: US/09/698,295
CURRENT FILING DATE: 2000-10-27
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APPLICANT: Nauert, Brian J.,
APPLICANT: Klauck, Theresa M.
APPLICANT: Klauck, Theresa M.
APPLICANT: Nauck, Theresa M.
AMBER OF INVENTION: Protein Binding Domains of Gravin
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEADTIME PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/769,309A
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PRIOR APPLICATION NUMBER: PCT/JP99/02340
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: JAPAN 10/137631
PRIOR PILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2907
                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 125; 20.7%; Pred. No. 0
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Patent No. 5741890
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                    99; Conservative
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity 18.9%; Pred. No. 0.11;
Matches 152; Conservative 96; Mismatches 237;
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5741890and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 amino acids
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MOLECULE TYPE: protein
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TELEFAX: 31
TELEX: 25-3
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517 PDHSSG----
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APPLICANT: Nauert, Brian J.,
APPLICANT: Klauck, Theresa M.
APPLICANT: None J.,
ADDRESSE: All J. O'Toole, Gerstein, Murray & Botheresse: Marshall, O'Toole, Gerstein, Murray & Botheresse: Marshall & Botheresse: Marshall & Botheresse: Marshall & Botheresse: Marshall & Bot
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,570
FILING DATE:
CLASSIFICATION:
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NAME: No. 6090929and, Greta E.
REGISTRATION NUMBER: 35,302
REPERENCE/DOCKET NUMBER: 27866/33451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                       969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
PEHREKMFNRLRIESKDLLLYSNV
                                                                                                                                                                                                                                   Sequence 5, Application US/08994570 Patent No. 6090929 GENERAL INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
                                                                                                                                                                                                      US-08-994-570-5
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1201 LÝPVRGTEAEAVPAQXERPPAPSSFVFQEETKEQSKMEDTLEHTDKEVSVETVSILSKTE 1260
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|1499 EGEKTTSLKWKS----DEVDE---
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Search completed: September 16, 2005, 10:47:19 Job time : 20.798 secs

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Sequence 98, App Sequence 130, A Sequence 15, Ap

Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1357, Ap Sequence 1355, Ap Sequence 1356, Ap Sequence 1024, Ap

Sequence 316809, Sequence 1, Appl Sequence 1, Appl Sequence 182739, Sequence 262, Appl Sequence 262, Appl

8429, Ap 2, Appli 684, App 316809,

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Sequence 501, App Sequence 2964, Ap Sequence 4, Appli Sequence 2, Appli

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Title: Perfect score:

Sequence:

protein

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Run on:

Scoring table:

Searched:

Database

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7 US-10-425-114-66899
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Sequence 3, Appli
Sequence 90, Appli
Sequence 7, Appli
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Sequence 2, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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3710
1 METGTHRARKRPGPRLGSWF......MFNRLRIESKDLLLYSNVKK
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(c) 1993 - 2005 Compugen Ltd.
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S US-10-650-482-2
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US-09-052-753-3
S US-10-277-603-3
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Sequence 490, App Sequence 14, Appli Sequence 141397, Sequence 7, Appli Sequence 7, Appli Sequence 122, App Sequence 122, App Sequence 127, App Sequence 10, Appli Sequence 1181, Appli Sequence 15014, Sequence 219612, Sequence 219612, Sequence 340752, Sequence 340752, Sequence 52303, A Sequence 52303, A Sequence 52303, A Sequence 3777, App Sequence 3777, Appli Sequence 52303, A Sequence 247745, Sequence 247745, Sequence 247745,

Sequence 54526, A Sequence 54526, A Sequence 51, Appl Sequence 48, Appl Sequence 44(1, Appl Sequence 3401, Appl Sequence 3401,

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Result è S Sequence 1618, A Sequence 303359, Sequence 22159,

Sequence 7, Appli Sequence 79, Appli Sequence 7, Appli Sequence 73, Appli

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Sequence 2, Application US/10650482
Sequence 2, Application US/10650482
Publication No. US20040142345A1
GENERAL INFORMATION:
APPLICANT: Ron, David
APPLICANT: Ron, David
APPLICANT: Ron, David
APPLICANT: Ron, David
APPLICANT: Soline
TITLE OF INVENTION: METHODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN eIFZalpha-SE
TITLE OF INVENTION: PHOSPHATASE SUBUNIT
FILE REFERENCE: 5986/1L/12-US1
CURRENT APPLICATION NUMBER: US/10/650,482
CURRENT APPLICATION NUMBER: US 60/408,679
PRIOR PILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 713
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                                                                                     DNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRI
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Best Local Similarity 65.0<sup>3</sup>
Matches 456, Conservative
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                                                                             1389, Ap
211, App
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US-10-408-765A-2821
US-10-128-58-234
US-10-128-58-234
US-10-369-493-1389
US-09-853-079-211
US-10-294-443-211
US-10-294-443-227
US-10-294-443-227
US-10-294-66-050A-671
US-09-866-050A-671
US-10-732-933-13576
US-10-437-963-13576
US-10-094-106-23
US-10-994-106-23
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Matches 698; Conservative
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LOCATION: (265)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (271)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                      186 SRLYSNRELGSSPSGLLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQ 245
                                                                                                 TITPESSCLREDHCHPQPLXAELIPXSWGCPPLSTEGLPEIHHLRMKRLEFLQQASKGQ 305
                                                                                                                                                                          | :|| ||||||||||| 366 VPLALLEESSPSEGCPSSEIPWEKEPGERISVVDYSYLEGDLPISARPACSNKLIDYILG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP----EPTEKKPELVIQE 361
                                                                                                                                                                                                                                 362 V----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILG 416
                                                                                                                                                                                                                                                                                                               GAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCR 655
                                                                             TLTPESCYLSEDGCHPOPLRAEMSATAWRRCPPLSTEGLPEIHHRRWRWLVPL-OPNOGO
                                                                                                                                                                                                                                                                                                                                     SIKLMNSFCNSDDPYNPLNFKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQL
187 AGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYLDYLPQLGLRCQSSAGGGQFVGFR
                                                                                                                                                                                                                                                                                                                                                                                            477 FTATIQTAARIAPRDPSDSGTSWSGSCGV-GSCQEGPLPETPDHSSGEEDDWEPSADEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         536 NLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQL
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j. Sequence 941, Application US/09925299

j. Publication No. US20030040617A9

j. GENERAL INFORMATION:

j. APPLICANT: Rosen et al.

j. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

rITLE OF INVENTION: Number: 180/09/925,299

CURRENT APPLICATION NUMBER: DCT/US00/05883

PRIOR PILING DATE: 2001-08-10

PRIOR FILING DATE: 1999-03-12

NUMBER: OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 941

LENGTHE: 707
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OTHER INFORMATION: Xaa equals any of the naturally
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (265)
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                        420 ACSNKLIDYILGGASSDLETSSDPEGEDWDEBAEDDGFDSDSSLSDSDLEQDPEGLHLWN 479
                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (271)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLD-S 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAPTFLLEQQLWGVELLPSSLQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDDWEPSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFS 583
                                                                                                                                                                                                                                                                                                                 584 GHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRK 643
                                                                                                                                                                                                                                                                                                                                   naturally occurring L-amino acids
  PTEKKPELVIQEV-----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP 404
                                                                                                                                                        SFHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSGSCGV-GSCQEGPLPETPDHSSGE 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 91, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INPORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAIOZ
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR RILING DATE: 2000-03-08
; PRIOR PILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PATENTIN VEY: 2.0
; SEQ ID NO 941
; LENGTH: 707
                                                                                                                                                                                                                                                                                                                                                                                                                  GPWEEFARDGCRFOKRIQETEVAIGYCLAFEHREKMFNRLR 684
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LOCATION: (265)
OTHER INFORMATION: Xaa
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US-09-925-299-941
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548 DPYNLLNFKAPFQPSGKOWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCG 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEAAALLTPTPVSGNL-LPHGETEESGSP-----EQSQAAQRLCLVEAESSPP---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLG-----NFKVVSY---LLN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ETWGLSNVDEYNAKPGQDDLREKEMERTAGKATLQPAGLQGADKRLGEVVAREEGVAE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSYLDYLPQLGLRCQSSAGGGQFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 PAY------PTSQLEGGPAEN------EEDGETVKTYQASAASIAPGYKPS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 YTAAGLFAKTRVVSTLALARG-----GTPVAVLVLRLEVKLKAQERAL---DSAAPTFLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVSPAADRP----EPTEKKPELVIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRG 395
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                                         4 DPYNPLNPKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSV
                                                                                                    -----AKTVTGADQ
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                                                                                 508 IGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEVAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 168; Gaps
                                                                                                                                                                                                                                                             Sequence 3, Application US/09052753A
Patent No. US20010014734A1
GENERAL INFORMATION:
APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: PROGRESSION ELEVATED GENE-3 AND USES THEREOF
FILE REPREBRUE: 0575/51523-B/JPW/JSG
CURRENT APPLICATION WHERE: US/09/052,753A
CURRENT FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%; Score 204; DB 9; 21.5%; Pred. No. 1.5e-06;
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Best Local Similarity 21.5*
Matches 149; Conservative
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US-09-052-753-3
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
FILE REPERBRUE: 784PCT
CURRENT PAPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/52,317
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
                                                                                   SELYSNRELGSSPSGLLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQ
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                 LLPSLFQKLLLWSQLSGGLIPTRWLDFAASYSALRASRGREESDAPTVQKSLSYTAAGLF
                                                                                                                                  127 AKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAPTFILLEQQLWGVELLPSSLQ
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Pred. No. 9.3e-34;
8; Mismatches 24; Indels
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Matches 105; Conservative 8
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ORGANISM: Homo
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US-10-296-115-963
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US-10-296-115-963
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LENGTH: 153
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: SPEQSQAAQRLCLVEAESSPP SSSSGPLSVQSLGNFKVVSY :: :: ERTAGKATLQPAGLQGADKRLGEVVAREE TLTPESCYLSEDGCHPQPLRAEMSATAWR
S6 IEAAALLTPTPVSGNL-LPHGETEESGSPEQSQAAQRLCLVEAESSPP 172 EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLGNFKVVSYLLN 173 EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLGNFKVVSYLLN 103ETWGLSNVDEYNAKPGQDDLREKEMERTAGKATLQPPAGLQGADKRLGEVVAREEGVAE 220 PSYLDYLPQLGLRCQSSAGGGGVVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPP

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Ob Company AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | : : | | | : EBEGVNKFSYPPSHRECCPAVEEEDDEBAVKKEAHRTSTSA 210
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                                                                                                RYTHIKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFAR 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL---- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
DIEDDIEEEEDSENVAPGDSETADSSQSPC------ 478
                                  DSKASSEVTVAFSGHH------TLLSCKAQLLES-- 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 186.5; DB 16; Length 674;
Pred. No. 3.4e-05;
3; Mismatches 270; Indels 227; Gaps
                                                                                                                                                                  S/10/755,889
-13
. 60/440,068
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	RESULT 10 US-10-277-603-7 Sequence 7, Application US/10277603 Publication No. US20030219376A1 GENERAL INFORMATION: APPLICANT: Fisher, Paul B. TITLE OF INVENTION: PROGRESSION ELEVATED GENE-3 AND USES TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF FILE REFERENCE: A34608-B-A CURRENT PELING DATE: 1096-B-A CURRENT FILING DATE: 2002-10-22 PRIOR APPLICATION NUMBER: 09/052,753 FRIOR APPLICATION NUMBER: PCT/US98/05793 PRIOR PILING DATE: 1998-03-30 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 578 TENGRIES FRI	Query Match A.94; Score 182.5; DB 15; Length 578; Best Local Similarity 22.7%; Pred. No. 5.5e-05; Indels 169; Gaps 28; Matches 130; Conservative 61; Mismatches 213; Indels 169; Gaps 28; Conservative 61; Mismatches 213; Indels 169; Gaps 28; Conservative 61; Mismatches 213; Indels 169; Gaps 264 Conservative 61; Mismatches 213; Indels 169; Gaps 264 Conservative 61; Mismatches 213; Indels 169; Gaps 264 Conservative 61; Mismatches 213; Indels 169; Gaps 265 LBABMSATARREC
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Query Match
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Fatent No. US20010014734A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE REFERENCE: 0575/51523-B/JPW/JSG
CURRENT APPLICATION NUMBER: US/09/052,753A
CURRENT FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIN Ver. 2.1
LENGTH: 590
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18.1%; Pred. No. 0.00039;
tive 68; Mismatches 198;
                                                                                                    DGCRFOKRIQETEVAIGYCLAFEHREKMFNRLR 684
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US-10-277-603-2
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Best Local Similarity 18.1%
Matches 100; Conservative
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163 SHW------BGCPSEEEEBDGETVKKAFRASADSPGHKSSTSVYCPGEAEHQATEEKQ 213
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18.1%; Pred. No. 0.00039;
tive 68; Mismatches 198; Indels 187;
                   GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEREOF
FILE REFERENCE: A34608-B-A
CURRENT APPLICATION THEREOF
CURRENT APPLICATION NUMBER: 09/052,753
PRIOR PILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 590
TYPE: PRI
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
Publication No. US20030219376A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 18.1% Matches 100; Conservative
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US-10-425-114-38378
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US-10-277-603-2
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TYPE: PRT
ORGANISM: Zea mays
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yorduc, David K.
APPLICANT: Cao, Yorduc, Yihua
APPLICANT: Cao, Yorduc, Yorduc,
                 APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Diants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 LPTLDQ----DNGYHSL----EEEHNLLRMD---PQHCTDNPAQAVSPAADRPEPTEKKP 355
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4.1%; Score 152.5; DB 15; Length 612;
Best Local Similarity 21.5%; Pred. No. 0.012;
Matches 90; Conservative 59; Mismatches 133; Indels 137;
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LOCATION: (1)..(661)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-425-114-38378
       Screen, Steven E
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ORGANISM: Zea mays
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APPLICANT: Thou, Yihua APPLICANT: Con, Yihua APPLICANT: Cond., Yihua APPLICANT: Screen, Steven E APPLICANT: Screen, Steven E APPLICANT: Screen, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REPERENCE: 38-21(5313)8 CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 66899
LENGTH: 830
                                                                                                                                                                                                                                                                                                             307 LPTLDQ----DNGYHSL----EEEHNLLRMD---PQHCTDNPAQAVSPAADRPEPTEKKP 355
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Best Local Similarity 21.5%; Pred. No. 0.013;
Matches 90; Conservative 59; Mismatches 133; Indels 137;
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US-10-425-114-66899
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US-10-425-115-207028
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
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114 ILGGAPSDLEASSDSESEDWGEE 104	414 ILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYK 473	474 PQNFTATIQTAARIAPRDPSDSGTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWE 528	529 PSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDS-KASSEVTVAFSGHHT 587	588 LLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKYT 626 :	627 FLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREKMFNRLRI 685
4 4 4 4 11 4 11 1 4 1	414 ILGGAPSDLEASSDSESEDWGEEI : : 604VSFNSKNEP	474 PONFTATIQTAARIAPRDPSDSG:	529 PSADEARNLKLWNSFCHSEDPYNI G78 QTAASVE	588 LLSCKAQLLESQEDNCPGCGLGEA :	627 FLEBUTEXYISGDEDRKGPWEEF/ : : : : 771 FTDDEDDMMLVGDDPWDEF

Search completed: September 16, 2005, 11:04:31 Job time: 239.943 Bec8

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Title: Perfect score: Sequence:

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Sequence 90, Appl Sequence 11494, A Sequence 90, Appl Sequence 90, Appl

Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 55843, A Sequence 31529, A Sequence 38378, A Sequence 207028, Sequence 207028, Sequence 58227, A Sequence 66899, A Sequence 66899, A Sequence 66899, A Sequence 77834, A

Sequence 733, App Sequence 152, App Sequence 152, App Sequence 1354, Ap Sequence 704, App Sequence 867, App Sequence 867, App Sequence 439, App

Sequence Sequence

SUMMARIES

Sequence 4, Appli Sequence 2316, A Sequence 18965, A Sequence 18965, A Sequence 2348, Ap Sequence 2348, Ap Sequence 941, App Sequence 941, App Sequence 963, App Sequence 15743, A Sequence 15743, A Sequence 15743, A Sequence 3, Appli Sequence 1651, Ap Sequence 1652, App Sequence 1652, App Sequence 1652, App Sequence 1653, App Sequence 1652, App Sequence 23269, App Sequence 18860, App Sequence 11652, A Sequence 18860, App Sequence 11651, A Sequence 11651, A Sequence 14551, A Sequence 14551, A Sequence 14551, A Sequence 1888, Ap

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Sequence 2, Application US/10650482
; Sequence 2, Application US/10650482
; Sequence 2, Application US/10650482
; GARERAL INFORMATION:
    APPLICANT: Ron, David
    APPLICANT: Souse, Celine
; TITLE OF INVENTION: WETHODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN elF2alpha-Si, TITLE OF INVENTION: PHOSPHATASE SUBUNIT
; TITLE OF INVENTION: PHOSPHATASE SUBUNIT
; CURRENT APPLICATION NUMBER: US/10/650,482
; CURRENT APPLICATION NUMBER: US 60/408,679
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; SEQ ID NO 2
; LENGTH: 713
                             DLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTAT 480
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llarity 65.0%; Pred. No. 7.8e-184;
Conservative 53; Mismatches 174;
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US-10-650-482-2
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Best Local Simi
Matches 456;
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US-10-650-482-2
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Sequence 4, Application US/10650482

Sequence 4, Application US/10650482

GENERAL INFORMATION:
APPLICANT: Jouse, Celine
TITLE OF INVENTION: WETHOODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN eIF2alpha-5
TITLE OF INVENTION: PHOSPHAYASE SUBUNIT
TITLE OF INVENTION: PHOSPHAYASE SUBUNIT
TITLE OF INVENTION: PHOSPHAYASE SUBUNIT
CURRENT APPLICATION NUMBER: US/10/650,482

CURRENT APPLICATION NUMBER: US 60/408,679
PRIOR APPLICATION NUMBER: US 60/408,679
PRIOR PRIOR PILING DATE: 2002-09-06

NUMBER: OF SEQ ID NOS: 10

SEQ ID NO 4
                                            Sequence 17386, A Sequence 22564, A Sequence 22564, A Sequence 10486, A Sequence 10486, A Sequence 10486, A Sequence 23688, A Sequence 23688, A Sequence 10485, A Sequence 10485, A Sequence 10485, A Sequence 36, Appl Sequence 310, Appl Sequence 310, Appl Sequence 38, Appl Sequence 1542, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
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US-60-191-637-13574
US-60-191-681-10700
US-00-19-681-10700
US-10-917-681-10786
US-10-917-503-17386
US-10-170-205B-22564
US-60-452-680-17245
US-60-453-135-10486
US-60-453-135-10486
US-10-755-889-36
US-10-755-889-36
US-10-755-889-36
US-60-453-050-11485
US-60-453-050-11485
US-60-453-050-11485
US-60-453-050-11485
US-60-453-050-11485
US-60-453-135-10485
US-60-453-135-10485
US-60-453-136-130
PCT-US01-29288-130
PCT-US02-2532-15
US-10-490-09-1542
PCT-US02-26322-15
US-10-490-09-21-15
US-10-490-09-21-15
US-10-490-09-21-15
US-10-490-09-21-15
US-10-490-09-21-15
US-10-480-09-21-15
US-10-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
          Best Local Similarity 100.
Matches 698; Conservative
                       TYPE: PRT
ORGANISM: Mus musculus
          LENGTH: 698
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APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE PASLES PASLES OF WINDOWS Version 4.0
SEQ ID NO 17655
LENGTH: 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||| SSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQ 179
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Best Local Similarity 64.9%,
Matches 455; Conservative
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GENERAL INFORMATION:
APPLICANT: ADDMS, Mark
TITLE OF INVENTION: DEFUCES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
CURRENT APPLICATION UNMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 23916
LENGTH: 713
                                                                                                                                                                                                                                                             360 STEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARP 419
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Best Local Similarity 64.9
Matches 455; Conservative
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ORGANISM: Homo sapiens
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US-10-170-205E-23916
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## APPLICANT: SAITO, KKOJI
## APPLICANT: SAITO, KKOJI
## APPLICANT: SAITO, KNOJI
## APPLICANT: SAITO, KNOJI
## APPLICANT: SUGIYAMA, TOMOYASU
## APPLICANT: SUGIYAMA, TOMOYASU
## APPLICANT: SUGIYAMA, TOMOYASU
## APPLICANT: WAKAMATSU, AI
## APPLICANT: WAKAMATSU, AI
## APPLICANT: OTSUKI, TETSUJI
## APPLICANT: NUMBER: US/09/629,469A
## PRIOR PILING DATE: 1999-07-28
## PRIOR PILING DATE: 1999-07-21
## PRIOR PILING DATE: 2000-01-11
## PRIOR PILING DATE: 2000-01-11
## PRIOR PILING DATE: 2000-05-02
## PRIOR PILING DATE: 2000-05-02
## PRIOR PILING DATE: 2000-05-01
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LWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQ
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APPLICANT: ISOCAL, TAKAO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HAYASHI, KOJI
APPLICANT: SATIO, KAORU
APPLICANT: SANIO, KAORU
APPLICANT: ISHIO, SHIZUKO
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US-09-629-469A-18965
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APPLICANT: YAMMOTO, JUNICHI
APPLICANT: YAMMOTO, JUNICHI
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: WAKAMATSU, AI
APPLICANT: MAKAMATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: OTSUKI, TETSUJI
FILLE REFERENCE: 084335/0123
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; Pred. No. 5.8e-183;
55; Mismatches 174;
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GENERAL INFORMATION:
APPLICANT: OTA, TOSHIO
APPLICANT: ISCGAI, TAKAO
APPLICANT: HAYASHI, KOJI
APPLICANT: SAITO, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SITIO, SHIZUKO
APPLICANT: SIGNIYAMA, TONOYASU
APPLICANT: SUGNIYAMA, TONOYASU
APPLICANT: WARAMATSU, AI
APPLICANT: WARAMATSU, AI
59.6%;
64.8%;
                                              Conservative
                       Similarity
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                  Local Simi
hes 454;
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Query Match
Best Local Similarity 64.8<sup>†</sup>
Matches 454; Conservative
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US-09-757-028-2348
                                                                                                       US-09-757-028-2348
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64.8%; Pred. No. 5.8e-183;
ive 55; Mismatches 174;
CURRENT APPLICATION NUMBER: US/10/917,503
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US/09/629,469
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1909-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-06-27
PRIOR PILING DATE: 1999-08-27
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PATENTIN VET. 2.1
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Best Local Similarity 64.8
Matches 454; Conservative
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US-10-917-503-18965
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                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PMO01
CURRENT APPLICATION NUMBER: US/09/757,028
CURRENT PILING DATE: 2001-01-09
FRIOR APPLICATION NUMBER: 60/179,065
FRIOR APPLICATION NUMBER: 60/180,628
FRIOR FILING DATE: 2000-01-01
FRIOR APPLICATION NUMBER: 60/180,628
FRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFWRARE: PATCHILIN Ver. 2.0
SEQ ID NO 2348
LENGTH: 720
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644 GPWEBFARDGCRFQKRIQETEVAIGYCLAFEHREKMFNRLR 684
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64.8%; Pred. No. 1.6e-182;
iive 54; Mismatches 175;
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; GENERAL INFORMATION:
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Best Local Similarity 64.8<sup>†</sup>
Matches 454; Conservative
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; ORGANISM: Homo sapiens
US-10-222-911-2348
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US-10-222-911-2348
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APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Human Colon Cancer Associated Gene Sequences and Polypeptides
TITLE OF INVENTION: Human Colon Cancer Associated Gene Sequences and Polypeptides
FILE REPERRINCE: PAIO2PCT
CURRENT PLILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 941
LENGTH: 707
                            246
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GHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (307); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino PCT-US00-05883-941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (271)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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                                                                                                                     GPWEEFARDGCRFOKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                                                                                                                                        GPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 707
                                                                                                                                                                                                                                                                                                                            Sequence 941, Application PC/TUS0005883; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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LOCATION: (265)
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NAME/KEY: SITE
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NAME/KEY: SITE
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366 VPLALEEESPEGCPSSEIPWEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILG 425
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                    246 TLTPESSCLREDHCHPQPLXAELIPXSWQGCPPLSTEGLPEIHHLRMKRLEFLQQASKGQ
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                                                                     DLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP----EPTEKKPELVIQE
                                                                                                                                             V----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILG
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Best Local Similarity 76.6%; Pred. No. 1.4e-38;
Matches 105; Conservative 8; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 FOKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 963, Application PC/TUS0035017A; GENERAL INFORMATION:
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US-10-296-115-963
; Sequence 963, Application US/10296115
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ORGANISM: Homo
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (271)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                       426 GASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQN 485
                                                                                                             536 NLKLWNSPCHSEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQL 595
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                                                                                                                                                                                                                                    LESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCR 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-941
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                  GAPSDLEASSDSESEDWGEEPEDDGPDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQN
                                                                                        PTATIOTAARIAPRDPSDSGTSWSGSCGV-GSCORGPLPETPDHSSGEEDDWEPSADEAE
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 941, Application US/09925299
Sequence 941, Application US/09925299
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA.0.2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 941
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Best Local Similarity 64.2
Matches 442; Conservative
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FEATURE:
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FILE REFERENCE: CL000456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 7356
LENGTH: 67
  TITLE OF INVENTION:
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9.6%; Score 357; DB 1; Length 101;
Best Local Similarity 75.0%; Pred. No. 2.7e-22;
Matches 66; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 15743, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT PEPLICATION NUMBER: PCT/US01/14827
; CURRENT PILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SEQ ID NO 15743
; LENGTH: 101
            APPLICANT: Hyseq Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPERENCE: 784PC.
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR PILIATION NUMBER: 1089/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-25
RIOR PILING DATE: 2000-01-25
SEQ ID NOS: 1478
SEQ ID NOS: 1478
                                                                                                                                                                                                                                                                                                                                                                                         24; Indels
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Pred. No. 1.4e-38;
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.6%;
Matches 105; Conservative
                                                                                                                                                                                                                                                              TYPE: PRT
GRGANISM: Homo sapiens
US-10-296-115-963
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ORGANISM: Homo sapiens
PCT-US01-14827-15743
GENERAL INFORMATION:
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US-60-196-718-7356
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APPLICANT: Bonazzi, Vivien TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

; Sequence 7356, Application US/60196718; GENERAL INFORMATION:

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Sequence 4491, Application US/60177571
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: USOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0201
CURRENT APPLICATION NUMBER: US/60/177,571
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: PastSEQ for Windows Version 4.0
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2; Mismatches 2; Indels
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Job time : 182.581 secs
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8.3%;

Best Local Similarity 93.3%;

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                        ; ORGANISM: HUMAN
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316, App
11618, A
1059, Ap
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21, r. 12801, A 9450, Ap 258, App 58, Appl 56, Appl 52, Appl 12800, A 54, Appl 21, Appl 6978, Ap 209, App 37734, A 52303, A 73, Appl 54525, A 55775, A 120587, 166, App 51233, A 2434, Ap 13049, A 13050, A 57981, A 1328, Ap 222, App 8, Appli 8, Appli 34, Appl 6713, Ap 24, Appl 15765, A 16, Appl 49, Appl 2821, Ap 168, App 167, App 1176, App 176, App 9651, App 23, App 147, App 1345, App 1346, App 147, App 257, App 2557, App 1281, Ap 264, App 530, App 123990, 2237, Ap 2, Appli 2, Appl 33975, Sequence seq Sequence Seq PCT-USO5-21650-40
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                                                                                                              624 KVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.7%; Score 175.5; DB 7; Length 605; Best Local Similarity 21.6%; Pred. No. 0.0077; Matches 131; Conservative 61; Mismatches 203; Indels 211; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: rat/human chimera (artificial) amino acid sequence; OTHER INFORMATION: of rPEG-3 1-347 + hGADD34 422-674
US-11-040-219-5
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-11-040-219-5
Sequence 5, Application US/11040219
Sequence 5, Application US/11040219
GENERAL INFORMATION:
TITLE OF INVENTION: Chimeric tumor suppressor gene and
TITLE OF INVENTION: Drotein
FILE REFERENCE: 36351 (070050.2617)
CURRENT PELICATION NUMBER: US/11/040,219
CURRENT FILING DATE: 2005-01-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 DODNGYHSLEEEH--NLLRMDPQHC--TDNPAQAV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VEAGLEGEAR------TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 GSDKNP--GEEKAEEEGVAEEEGVNKFSYPPSHRECCPAVEEEDDEEAVKKEAHRTSTSA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 LSPGSKPSTWVSCPGBEENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE 270
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Sequence 768, App
Sequence 13260, A
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                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/11040219
GENERAL INFORMATION:
APPLICANT: Paul Fisher
TITLE OF INVENTION: Chimeric tumor suppressor gene and
TITLE OF INVENTION: Drotein
FILE REPRENCE: 36351 (070050.2617)
CURRENT RILING DATE: 2005-01-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: human GADD34 amino acid sequence
US-11-040-219-2
US-11-090-997-768
US-11-097-143-13260
                                                                                                                                            ALIGNMENTS
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ORGANISM: Homo sapien
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US-11-040-219-2
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2818 PTAEESAKERF--SLYQHQGGLGSQVSALPPNSLVRKVKRTLPSPPPEEAHLPLAGQDQL 2875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --QNGF----AEPGLPNQAPTYPGPSTYPAPAFPPGASYP----AEPGLPNQQAF 3070
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                        PETPDHSSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGKNWKGRQDSK
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4.1%; Score 151; DB 1; Length 3880;
Best Local Similarity 22.6%; Pred. No. 3;
Matches 150; Conservative 81; Mismatches 236; Indels 198;
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JAPPLICANT: DAVID WORTES
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JAPPLICANTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
JELER REPERENCE: CHIROGG--500 (23356,0003)
JUNIOR PRICE REPRENCE: CHIROGG--500 (23356,0003)
JENIOR APPLICATION NUMBER: PCT/US04/10-21
JENIOR APPLICATION NUMBER: US 10/692,382
JENIOR PRILING DATE: 2003-10-21
JENIOR FILING DATE: 2003-10-21
                                                                                                                                                                                                                                                                        ; Sequence 2439, Application PC/TUS0437982; GENERAL INFORMATION:
                                                 sapiens
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2980 LQGCTTPAGQFVDFPATA---AAPATPSGPTAFQQPR------FQPPAPQYSAGSGGPT- 3029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2769 LDTSFASSLNKAHVS----PQK--HFTAD-SALR----QQTLPRPMKTLQRSLSDPKPLS 2817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 --TFLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLN---- 219
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9 RKRPGP-RLGSWFRLPFLRRSHACSSEFPPPSSRQNPGNSALPERRTRYWTKLLSQLLAL 67
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
FILE REFERENCE: CHIROGO-500 (23356.003)
CURRENT APPLICATION NUMBER: PCT/US04/37982
CURRENT APPLICATION NUMBER: US 10/692,382
PRIOR PILING DATE: 2003-10-21
PRIOR APPLICATION NUMBER: US 10/691,209
PRIOR APPLICATION NUMBER: US 10/691,209
PRIOR APPLICATION NUMBER: US 3003-310-21
PRIOR PELING DATE: 2003-10-21
PRIOR PELING DATE: 2003-10-21
SOFTWARE: FREEEEC for Windows Version 4.0
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                                                                       679 MFNRLR 684
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LENGTH: 3880
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Db 364 VDGEDESTTEVSTSTTDKPEESSTTREPEEDSTTNGKPE-ESSTTTEQPEDSITTTEEPI 422 QY 378 EKECEDHTNATDLSDRGESLPVSTRPVCSTRICGAAPSDLEASSDSESEDWG- 434 Db 423 DSTTEAPEDESTTSSPTDGGEQSTTEEPETTTEKPEETSTSPIDTEDSTTKEPEDVST 480	481 TPKESEESTTSSPENDDTTSAPGEDDTTAAPGGDEESTTTEPPEETTTSPSDADDSTTE 473 KPQNFTATIQTAARIAPRDPSDSGTSWSGSCGVGSCGPLPETPDHSSGEEDDWE 541 EPEEDTTTKKPVEPSTTTEEPEDSTTEVPEESTTEEPDKE 529 FSADAE 535 582 TSTTNAE 588 SULT 6 583 TSTTNAE 588 SULT 6 584 TSTTNAE 588 SULT 6 585	Query March 3.8%; Scrole 140.5; DB 6; Length 9.16; Matches 166; Conservative 79; Mismatches 250; Indels 361; Gaps 36; Matches 166; Conservative 79; Mismatches 250; Indels 361; Gaps 36; Qy
	SULT 5 Sequence CENTERM Sequence CENTERM APPLIC TITLE TITLE TITLE FILLS FILLS FILLS FRICH PRICH	WINDER OF SEQ ID NOS: 43008-033

Qy 256 SEDGCHPQPLRAEMSATAWRRC	Qy 454 EQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDGTSWSGSC 503 Db 784 GQGAEGGLERVQNSLRRRTHS	EDMCNKLGIFRRRNESPGAPPAGKADKWAKSFRPTSBEALKWGESLEKLLVHKDGLAVFO SPCHSEDPYNLLNFKAPPQPSGKNWKGRQDSKASSBVTVAFSGHHTLLSCKAQ SPCHSEDPYNLLNFKAPPQPSGKNWKGRQDSKASSBVTVAFSGHHTLLSCKAQ H	SECTION OF 4	Query Match 3.8%; Score 139.5; DB 1; Length 883; Best Local Similarity 22.3%; Pred. No. 2.2; Matches 154; Conservative 66; Mismatches 217; Indels 253; Gaps 39; Qy 140 GGTPVAVLVLRLEYKIKADERALDSAAPTFLEQQLWGVELLPSSLQAGLVSHRE 194 Db
05 05 05 05 05 05 05 05	547 EDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAPSGHHTLLSCKAQLLES	RESULT 7 US-10-899-422-11 ; Sequence 11, Application US/10899422 ; GENERAL INFORMATION: APPLICANT: Lorantial limited TILLE OF INVENTION: Medical Treatment FILE REFERENCE: P020742US CLM CURRENT APPLICATION NUMBER: US/10/899, 422 CURRENT PILING DATE: 2004-07-26 PRIOR PILIOR DATE: 2002-01-25 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin version 3.0 SEQ ID NO 11 LENGTH: 1059 TYPE: PRT	ORGANISM: Homo sapiens US-10-899-422-11 ORGANISM: Homo sapiens US-10-899-422-11 Ouery Match US-8; Score 140.5; DB 6; Length 1059; Best Local Similarity 19.2%; Pred. No. 2.4; Matches 165; Conservative 82; Mismatches 243; Indels 371; Gaps 37; Matches 165; Conservative US-10-105WFR	354EBSGSPSKGKSYTGLGKKSRLMKTVQTMKGHGNYQNCPVVRPHATHSS 141 -GTPVAVLVLREVKLKAQERALDSAAPTFLLEQQLMGVELLPSSLQAGLVSHREL

LPERRTRYWTKLLSQLI	Db 188 LAPLNPGSQ 208	OY 99 ALRASRGREESDAPTVQKSLSYTAAGLFAKTRVVSTLALARG140	Db 209BESGSPSKGKSYTGLGKKSRLMKTVQTMKGHGNYQNCPVVRPHATHSS 256	Qy 141 -GTPVAVLVIRLEVKLKAQERALDSAAPTFILEQQLWGVELLPSSLQAGLVSHREL 195	257 YGTYVTLAPKVLVFPVFVQPLDLCNPARTLILISEELILYEGRNKAABVTLFAYSDLLLFT	196 DSSSSGPLSVQSLGNFKVVSYLLNPSYLDYLPQLGLRCQSSAGGGGVGFRTLTPESCYL	DD 3.17 KEDERGKCUVLKNPLYLQSVKLUEGSSEDLKK-UVL	354 AEKAECLFTLEAHSQEQKKRVCWCLSENIAKQQQLADPDSKWFETEADEKKEMALEEGKG	Cy 297VFLQPNQGQDL PTLDQDNGYHSLEBEHNLLRMD 329	Db 414 PGAEDSPPSKEPSPGGELPPGQDLPPNKDSPSGGEPAPSGEPLSSKDSATSEGSPPGPDA 473	Cy 330PQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCE 374	DD 474 PPSKDVPPCQEPPPAQDLSPCQDLPAGQEPLPHQDPLITKDLPAIQESPTRDLPPCQDLP 533	Cy 375CENTREACEEDHTNATDLSDRGESLPVSTRPVCSN 408	Db 534 PSQVSLPA-KALTEDIMSSGDLLAATGDPPAAPRPAFVIPEVRLDSTYSQKAGAEQGCS- 591	Cy 409 KLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEG- 459	Db 592GDEEDABEAEEVEGGEEGEBDBDTSDDNYGERSEAKRSSMIETGQGAEGG 643	Cy 460LHLWNSFHSVDPYKPQNFTATIQTAARIAPRDFSDSGTSWSGSCGVGSCQE 510	Db 644 LSLRVQNSLRRRTHSEGSLLQEPRGPCFASDTTLHCSDGEGAASTWG 690	Qy 511 GPLPETPDHSSGE	Db 691 MPSPSTLKKELGRNGGSMHHLSLFFTGHRKMSGADTVGDDDEASRKRKSKNL 742	Qy 546 SEDPYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQ 599 ::	Oy 600 EDNCPGCGLGEALAGERYTHIKRKKYTFLEEVTEYYISGDEDRK 643	Db 793 LVHKYGLAVFQAFLRTEFSEENLEFWLACEDFKK 826	RESULT 10	PCT-US04-37982-202 ; Sequence 202, Application PC/TUS0437982	; GENERAL INFORMATION: ; APPLICANT: DAVIG W. Morris ; APPLICANT: Over C. Wallandson	; AFFILCANI: MAIC S. MAIANGED OF STATES AND METHODS IN CANCER : FITHE REFERENCE: CHIROLOGO-SOO (23356,0003)	CURRENT APPLICATION NUMBER: PCT/US04/31982 CURRENT FILING DATE: 2004-10-21	FRIOK PILING DATE: 2003-10-20.	FRIOR FILING DATE: 2003-10-21, STATE OF	; SEQ ID NO 202 ; LENGTH: 913	; TYPE: PRI
Db 143 DDSSDAVEVKVKGVVFLYREGSARYAFSFAGAQEACARIGARIATPEQL-YAAYLGGYEQ 201	Cy 235 SSAGGGOFVGFRTLTP-ESCYLSEDGCHPQPLRAEMSA- 271	Db 202 CDAGWLSDQTVRYPIQNPREACYGDMDGYPGVRNYGVVGPDDLYDVYCYAEDLNGELFLG 261	Qy 272PLSTE 283	Db 262 APPGKLTWBEARDYCLERGAQIASTGQLYAÄWNGGLDRĊSPGWLADGSVRYPITHPSQRC 321	284GLPEIHHRRMRWIVFLQPNQGQDLPTLDQDNGYHSLBEEHNLLRMDPQHCTDNPA	322 GGGLPGVKTLPLFPNQTGFPSKQNRFNVYCFRDSAHPS	CY 3.59QAVSFAADREEFTEKKRELVI_QBVSQSPQSSELFCELFVEKECEEDHINATU 3.90 Dh 3.60 AFSFASSPASNGIRALVITYTEKTIREDIDIDORAVESSERGATV_SIDITE 4.07	391 LSDRGESLPVSTRPVCSNKLIDYILGGAP-SDLEASSDSESEDWGEEPEDDGFD		Cy 444 SDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRD 491	Db 455 KDTETPKEEKEQENLWVWPTELSSPLPTGLETEHSLSQVSPP-AQAVLQLGASPSPRP 511	Qy 492 PSDSGTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWEPSADEAENLKLWNSFCHSED 548	Db 512 PRVHGPPAETLQPPREGSLTSTPDGAREVAGBTGSPELSGVPRESEEAGSSSLED 566	Cy 549 PYNLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGH 585	Db 567 GPSLLPATWAPVGTRELETPSEEKSGRTVLTGTSVQAQPVLPTDSASRGGVAVAPSSG 624	Cy 586 HTLLS-CKAQLLESQED-NCPGCGLGEALAGERYTHIKRKKV 625	Db 625 DCIPSPCHNGGTCLEEKEGFRCLCLPGYGGDLCDVGLHFCSPGWEAFQGACYKHFSTRR- 683	Qy 626 TFLEEVTEYYISGDEDRKGPWEEFARDGCR 655	Db 684SWEE-AESQCR 693		RESULT 9 PCT-0304-37982-188 ; Sequence 188, Application PC/TUS0437982 ; GENERAL INFORMATION:	040	; TITLE OF INVESTION: NOVEE COMPOSITIONS AND METHODS IN CANCER; FILE REFERENCE: CHIROD62-500 (23356.0003); CURRENT APPLICATION NUMBER: PCT/USO4/37982	; CURRENT FILING DATE: 2004-10-21 ; PRIOR APPLICATION NUMBER: US 10/692,382	; PRIOR FILING DATE: 2003-10-22 ; PRIOR APPLICATION NUMBER: US 10/691,209	NUMBER OF SEQ ID NOS: 3504	; SOCIWARE: FABELSEQ IOI WINGOWS VEIBION 4.0 ; SEQ ID NO 188 : IRNGTH: 913	PE 22 0		Vact Fraction 19.3%; Prod. 100.2 bb 1; Leuglu 313; Best Local Similarity 19.3%; Pred. 100. 2.8; Matches 164; Conservative 84; Mismatches 266; Indels 310; Gaps 34;	5 THRARKRPGPRLGSWFRLPFLRKSHFRSPPPP	Db 128 THGVQARPEQRHSCHLVCDSSDGLLLGGWERYTEVAKRGGQHTLPALSRATAPTDPNYII 187

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191 | HPSPSTLKKELGRNGGSMHILSLFFTGHRKMSGADTVGDDDEASRKRKSKNL----- 742
                                                                                                                          THGVQARPEQRHSCHLVCDSSDGLLLGGWERYTEVAKRGGQHTLPALSRATAPTDPNYII 187
                                                                                                                                                                                                                                                                    -GTPVAVLVLRLEVKLKAQERALDSAAPTFLLEQQLWGVELLPSSLQAGLVSHREL---- 195
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                                                                                                                                                      SSRQNPGNSALPERRTRYWTKLLSQLLALLPSLFQKLLLWSQLSGGLIPTRWLDFAASYS 98
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                                                                      Gaps
                                                                    266; Indels 310;
                                        3.7%; Score 138; DB 1; Length 913; 19.9%; Pred. No. 2.8; ive 84; Mismatches 266; Indels 3
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS IN CANCER
PILE REPERBUCE: GHIRO62-500 (23356.003)
CURRENT APPLICATION NUMBER: PCT/US04/37982
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Best Local Similarity 19.9
Matches 164; Conservative

// ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---LGSWFR----
                                                                                                                                                                                                                                                                                                                                                                                                                        266;
                                                                                                                                                                                                                                                                                                                                                                     3.7%; Score 138; DB
19.9%; Pred. No. 3.6;
iive 84; Mismatches
PRIOR APPLICATION NUMBER: US 10/692,382
PRIOR PILING DATE: 2003-10-22
PRIOR PILING DATE: 2003-10-21
PRIOR APPLICATION NUMBER: US 10/691,209
PRIOR FILING DATE: 2003-10-21
NUMBER OF SEQ ID NOS: 3504
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 192
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Matches 164; Conservative
                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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APPLICANT: Raelson, John Verner
APPLICANT: Bradley, Walter Edward
APPLICANT: Bradley, Walter Edward
APPLICANT: Paquin, Bruno
APPLICANT: Fournier, Helene
APPLICANT: Nguyen-Huu, Quynh
APPLICANT: Croteau, Pascal
TITLE OF INVENTION: Genemap of the Human Genes Associated with Crohn's Disease
File Reference: 59908-5002-FR
CURRENT APPLICATION NUMBER: US/60/675,841
                                                                                                                                                                                                                                                     GDREVEVLVARGLRVKVNEAYRFRVALPAYPASLTDVSLVLÆBLRPNDSGVYRCEVQHGI 142
                                                                                                                                                                                                                           140 GGTPVAVLV---LRLEVKLKAQERALDSAAPTFLLEQQLWGVELLP--SSLQAGLVSHRE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDAGWLSDQTVRYPIQNPREACYGDMDGYPGVRNYGVVGPDDLYDVYCYAEDLNGELFLG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPA--- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AFSEASSPASDGLEAIUTVTEKLEELQLPQEAVESENVYAIY-SIPI-----TE 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSDSGTSWSGSCGVGSCQEGPLPETPDHS---SGREDDWBPSADEARNLXLWNSFCHSED 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 PYNLLNFKAPFQPSG------KWWKGR------QDSKASSEVTVAFSGH 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 HTLLS-CK--AQLLESQED-NC--PG-----CGLG------EALAGERYTHIKRKKV 625
                                                                                                                                                                                                                                                                                                                  --GNFKVVSYLLNPSYLDYLPQLGLRCQ 234
                                                                                                                                                                                                                                                                                                                                                            143 DDSSDAVEVKVKGVVFLYREGSARYAFSFAGAQEACARIGARIATPEQL-YAAYLGGYEQ 201
                                                                                                                                                                                                                                                                                                                                                                                                         235 SSAG--GGQFVGFRTLTP-ESCYLSEDG-------CHPQPLRAEMSA- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 APPGKLIWEEARDYCLERGAQIASTGQLYAAWNGGLDRCSPGWLADGSVRYPIITPSQRC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 GGGLPGVK-----TLFLFPNQ-----TGFPSKQNRFNV-----YCFRDSAHPS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---QAVSPAADRPEP----TEKKPELVI-QEVSQSPQGSSLFCELPVEKECEEDHTNATD 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGSLSESDVEQDSEGLHLW-----NSFHSVDPYKPQNFTATIQTAARIAPRD 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         567 GPSLL--PATWAPVGTRELETPSEEKSGRTVLTGTSVQAQPVLPTDSASRGGVAVAPSSG 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 DCIPSPCHNGGTCLEEKEGFRCLCLPGYGGDLCDVGLHFCSPGWEAFQGACYKHFSTRR- 683
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                                                                                                                                                                            253;
                                                                                                                               Length 883;
                                                                                                                                                                                Indels
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                                                                                                                                 ; Score 136.5; DB 1;
; Pred. No. 3.4;
66; Mismatches 217;
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                                                                                                                                    3.7%;
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                                                                                                                               Query Match
Best Local Similarity 22.3%;
Matches 154; Conservative
                                        TYPE: PRT
ORGANISM: Rattus sp.
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                                                                    ; ORGANISM: Rati
PCT-US05-01184A-3
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                       LENGTH: 883
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SEQ ID NO 3
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APPLICANT: Yale University
APPLICANT: Plackfield, Susan
APPLICANT: Matchwas, Russell T.
APPLICANT: Matchwas, Russell T.
APPLICANT: Wisplano, Mariano S.
TITLE OF INVENTION: PRIMARY CENTRAL NERVOUS SYSTEM TUMOR SPECIFIC BEHAB ISOFORMS
TITLE OF INVENTION: PRIMARY CENTRAL NERVOUS SYSTEM TUMOR SPECIFIC BEHAB ISOFORMS
CURRENT APPLICATION NUMBER: 2005-01-14
PRIOR PILING DATE: 2005-01-14
PRIOR PILING DATE: 2005-01-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.2
                                                                                                     APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO01495
CURRENT APPLICATION NUMBER: US/10/990,328A
CURRENT PILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11742
LENGTH: 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 LQFKVEVTSSVHEDASPEAVGTILGVNSVNGDLGSPSDDEDMPGSHHDSQVCSNGPVSED 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 SAA------DGTPKHSFRTSSTLE---IDTEELTSTSSRTSPPRGRQDSLN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 -YLS--EDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRWRWLVFLQPNQGQDLPTL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIQEVSQS--PQGSSLFCELPVEKECE---EDHTNATDLSDRGESLPVSTRPVCSNKLID 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQDNGY-HSLEEEHNLL-----RMDPQHCT-----DNPAQAVSPAADRPEPTEKKPEL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 YILGGAPS-----DLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PSDPARTESVSEASTR--PEGESDL-----ECADSSCNESVTTQLSSVDTRCS 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 LVLRLEVKLKAQERALDSAAPTFLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 NLPELAESSLPAG-----PAPEEGEGEPEPQPSA----DQGSA-----ELCGSQEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.7%; Score 138; DB 6; Length 1572;
22.9%; Pred. No. 5.8;
iive 43; Mismatches 167; Indels 134;
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                                                             Sequence 11742, Application US/10990328A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application PC/TUS0501184A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 22.99
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         US-10-990-328A-11742
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PCT-US05-01184A-3
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APPLICANT: Croteau, Pascal
APPLICANT: Croteau, Pascal
APPLICANT: Alrard, Rene
APPLICANT: Serie, Valerie
APPLICANT: Exdewegh, Paul V
APPLICANT: Little, Randall D
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the human genes associated with Crohn's disease
FILE REFERENCE: 059908-5009-PR
                                                                                                                                                                                                                           |||||:: | ::|:| :| | | | | | | ||:
LSQLVSRQPPKSPQ-VLYSPVS-PLSPHRLLDTSPASSERLNKAHVSPQKHFTADSALR- 2835
                                                                                                                                                                                                                                                                                             ---QQTLPRPMKTLQRSLSDPKPLSPTAEBSAKERF--SLYQHQGGLGSQVSALPPNSLV 2890
                                                                                                                                                                                                                                                                                                                                                         3052 QQPR-----PQPPAPQYSAGSGGPT---ONGF------PAHQAPTYPGPSTY 3089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2995 GGRDYPPLRGLGEHRDYLSDSELNQLRLQGCTTPAGQFVDFPATA---AAPATPSGPTAF 3051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3090 PAPAFPPGASYP----AEPGLPNQQAFRPTGHYAGQTPMPTTQSTLF-PVPADSRAPLQK 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3145 PRQTSLADLEQKVPTNYEVIASPVV---PMSSAPSETSYSGPAVSSGYEQGKVPEVPRAG 3201
                                                                                                                                                                                                                                                                    103 SRGREESDAP--TVQKSLS----YTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKL 155
                                                                                                                                                                                                                                                                                                                                     -----TPLLEQQLWGVELLPSSLQAGLVSHRELDSS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHRRMRWLVFLQP----NGGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDN----- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAQAVSPAADRPEPTEKKPELVIQE----VSQSPQ---GSSLFCELPVEKECEEDH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDW--GEEPEDDGFD 443
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                                                                                                                                                                                                                                                                                                                                                                                                    199 SSGPLSVQSLGNFKVVSYLLN------PSYLDYLPQLGL--RCQSSA---
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                                                                                                                                                                           Gaps
                                                                                                                                          Query Match
3.7%; Score 136.5; DB 8; Length 3926;
Best Local Similarity 23.9%; Pred. No. 24;
Matches 140; Conservative 68; Mismatches 199; Indels 179;
                                                                                                                                         Length 3926,
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CURRENT FILING DATE: 2005-04-29
WUMBER OF SEQ ID NOS: 10858
SOFTWARE: Patentin version 3.3
SEQ ID NO 94
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Bradley, Walter E
Paquin, Bruno
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                                                                                                                                                                                                                                                                                                                                     156 KAQERALDSAAP-
                                                              LENGTH: 3926
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                           US-60-675-841-94
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1052 QQPR-----FQPPAPQYSAGSGGPT---QNGF-------PAHQAPTYPGPSTY 3089
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                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SALRA 102
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                                                                                                                                                                                                                                                                                                                                                                                       Gape
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                                                                                                                                                                                                                                                                                                                           Length 3926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LSQLLALLPSLFQKLLLWSQLSGGLIPTRWLD--FAASY----
                                                                                                                                                                                                                                                                                                                        Query Match
3.7%; Score 136.5; DB 8;
Best Local Similarity 23.9%; Pred. No. 24;
Matches 140; Conservative 68; Mismatches 198;
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Job time : 86.5911 secs
CURRENT APPLICATION NUMBER: US/60/710,726
CURRENT FILING DATE: 2005-08-24
NUMBER OF SEQ ID NOS: 20166
SOFTWARE: PatentIn version 3.3
SEQ ID NO 316
LENGTH: 3926
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                                                                                                                                                                                                                           ORGANISM: Homosapiens
US-60-710-726-316
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model protein δ

September 16, 2005, 08:56:27 Run on:

7; Search time 17.8086 Seconds (without alignments) 3771.163 Million cell updates/sec

US-10-650-482-4 3710 1 METGTHRARKRPGPRLGSWF.....MFNRLRIESKDLLLYSNVKK 698 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 79:*
!: pirl:*
!: pir2:*
!: pir3:*
!: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SRP40 protein - ye protein phosphatas hypothetical prote ankyrin 3, long sp mismatch repair en hypothetical prote hypothetical prote hypothetical prote luminidependens pr MAKIG protein - ye homeotic protein H gravin - human faciogenital dyspl KIAA0633 protein -probable nucleopor hypothetical prote hypothetical prote hypothetical prote protein F56012.4 [hypothetical prote brevican precursor vlpe-like (mycopla hypothetical prote calcium-binding pr C-terminal domain-SRP40 protein - ye MyD116 protein - m gadd34 protein - l Formin - mouse Description SUMMARIES \$10001 A55035 A56036 T40520 T40520 T70062 P9062 % Query Match Length DB 0.057 15.50 10.527 121.5 120.5 120.5 120.5 119.5 119.5 1119.5 1119.5 204 171.5 151.5 161.5 114.5 114.5 1136.5 1130.5 1120.5 126.5 127.5 127.5 123.5 Result No.

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                                                                              RESULT 1
$10001
MyD116 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Musculus (house mouse)
Nucleic Acids Res. 18, 2823, 1990
A;Title: Sequence of MyD116 cDNA: a novel myeloid differentiation primary response gene
A;Reference number: $10001
A;Molecule type: mRNA
A;Residues: 1-657 <LDR>
A;Residues: 1-657 <LDR>
A;Cross-references: UNIPROT:P17564; EMBL:X51829; NID:g53040; PIDN:CAA36128.1; PID:g53041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 IEAAALLTPTPVSGNL-LPHGETEESGSP-----EQSQAAQRLCLVEAESSPP---- 102
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RESULT 2 A56535

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gadd34 protein - long-tailed hamster
N;Alternate names: MyD116 protein homolog
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56535
R;Zhan, Q; Lord, K.A.; Alamo Jr., I.; Hollander, M.C.; Carrier, F.; Ron, D.; Kohn, K.W.
Mol. Cell. Biol. 14, 2361-2371, 1994
A;Title: The gadd and MyD genes define a novel set of mammalian genes encoding acidic pr.
A;Reference number: A56535 MUID:94187707; PMID:8139541
A;Accession: A56535
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 1-590 <ZHA>
A;Cross-references: UNIPROT:Q60465; GB:L28147; NID:g452489; PIDN:AAA36983.1; PID:g452490
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---STEGLPEIHHRR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YHSLEEEH 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 SHW-----EGCPSEEEEDGETVKKAFRASADSPGHKSSTSVYCPGEAEHQATEEKQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DT------BDDQDSDWGSAEKDGLAQTFATPHTSAFLKTWVCCPGEDTEDDDC 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 EVVVPEDSEAADPDKSPSHEAQGCLPGEQTEGL-----VEAEHSLFQVAFYLPGEKPAP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKK 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 VIFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFOKRIOETEVAIGYCLAFEHREKM 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 NLLRMDP------TEKKPELV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 TENKADPPSSPSGSHSRAWEYCSKOEGEA-----DPEPHRAGKYOLCONAEAEEEERAK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 IQEVSQSPQGSSL--FCELPVEKECEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WVYRPGEDTEDDDDSDWGSAEE-----EGKALSSPTSPEHDFLKAW------VYRPGE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- PDHSSGEEDDWEPS-----ADEAENLKLWNSFCHSEDPYNLLNFKAPFQPSGK 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 PW-----TAPKLPLRLQRRLTLLRTPTQ---DQDPETP------LRARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590;
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
C;Accession: T33100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 FTATIOTAARIAPRDPSDSGTSWSGSCGVGSCOEGPLPET----
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submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid H11E01
A;Reference number: 221282
A;Accession: T33100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein H11E01.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 171.5; DB 2;
llarity 18.1%; Pred. No. 0.00069;
Conservative 68; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 MRWLVFLQPNQGQDLPTLDQDNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 PESCYLSEDGCHPQPLRAEMSATAWRRCPPL-
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A;Rezidues: 115.2 <LYN>
A;Rezidues: 1222 <LYN>
A;Cross-references: UNIPROT:059740; EMBL:AL023634; PIDN:CAA19170.1; GSPDB:GN00067; SPDB:£
A;Experimental source: strain 972h-; cosmid c530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSTSEDI-SIEGSPSETAKG--ARSFNSNFRTFDIGS------ERRRRILEASQDS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | | | | : | | : | | 17 VLDPDGDAYVNRYARPVTAGSIYIPSNYHKSFSPNTFSGFNVKR-----SASKSPKRSAN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AAPTFLLEQQLWGVELLPSSLQAGLVSHRELDSS---SSGPL--SVQSL--GNFKVVSYL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 VPDMSSPVPASSVEYESLKAAVTYSPSQNPKKVAETDSESRKSSFQSSYN-----DA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : : | | : | : : | | : | : : | 371 AISQSMRSFQPQPIT -----GSPPPRTSTNTEDEQESDIPQSDANDSTVNLNQPNY - 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ALPERRIRYWIKLLSQLLA---LLPSLFQKLLLWSQLSGGLIPTRWLDFAASYSALRASR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREESDAPTVQKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 INPSYLDYLPQLGLRCQSSAGGQPVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 PPLSTEGLP--EIHHRRMRWLVFLQPNQG-QDLPTLDQDNGYHSLEEEHNLLRMDPQHCT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 DRPPQVGAQTQSTPNRISRSDSPIVYDVDTH-------SED--NASTASSE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 GESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVE 454
                                                                                                     Aypothetical protein SPBC530.04 - fission yeast (Schizosaccharomyces pombe) C, Species: Schizosaccharomyces pombe C, Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypochetical protein KIAA0434 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Jan1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETSELSKKPRPNTTVGFOFDNRNVGTSAPSTPAIRRNNTDSFERGLSLPLPSSKODTGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ETGTHRARKRPGPRLGSWF-----RLPFLRRSHACSSE----FPPPSSRQNPGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRP-----GRYSYRTKSASPALIDISTLDSRLNFTMGRLERSIAQLSKNTMRAVSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSGSCGVGSCOEGPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 141; DB 2; Length 522;
20.8%; Pred. No. 0.07;
Live 78; Mismatches 229; Indels 138; Gaps
                                                                                                                                                                                                              Barrell, B.G.; Rieger, 1998
                                                                                                                                                                                          C;Accession: T40520

%Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.C

submitted to the EMBL Data Library, May 1998

A;Reference number: 221934

A;Accession: T40520

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: SPDB:SPBC530.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
A; Introns: 20/3
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1510 cGE1>
A;Cross-references: UNIPROT:061802; EMBL:AF067222; PIDN:AAC17017.1; GSPDB:GN00028; CESP:A;Experimental source: strain Bristol N2; clone H1E01
C;Genetics:
A;Gene: CESP:H1E01.3
A;Map position: X
A;Introns: 73/2; 120/1; 178/3; 227/2; 262/1; 300/2; 345/1; 1430/3; 1468/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 EQEEQEFIPRQIVLDNADPSHGDYEDSDSEPEYAEEDREPLAVQVQLEHQVD----- 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEGPLPETPDH-----SSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNFK 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PHVSEHPEHHEEAQHSPVASQEEAARSPSVHSSHASEHFEHHEEAQDSPVASQEK 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | : :||: 862 AARSPSVHSSHASEDSERIENHGESLQSPVA 921
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                                                                                                                                                                                                                                                                                                                                                                                                                          | | ::| |: || : || GPHSVARQPPPQQASWF---FRRRSVLNWRGRKATTGNKLNASHDSRTSCPPTTRKKDS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALRASRGREESDAPTVQKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | : | 375 EPEPSPPRTPVLETQKTFDRTSPTD-----GVQVPDEVPPBILDKLADESEDVEEKLA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LPQLGLRCQSSAGGGQFVG 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 TITSVSKSPQISDTNTLPTLPSVTGRGIFTGAAAATAA-----AIGTAAINMDTLIDK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q------ERALDSAAPTFLLEQQLWGVEL---LPSSLQAGLVSHRELDSSSSG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537 APESPNEVVHHVQ-----TEAQOSPVIDVHSTHVVEHFDTHDESPQSPVLSVHGGE 587
                                                                                                                                                                                                                                                                                                                                                                                     ----SHACSSEPPPSSRQNPG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSALP---ERRTRYWTK-----LLSQLLALLPSLFQKLLLWSQLSGGLIPTRWLDFAASY
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                                                                                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                         Query Match
4.1%; Score 151.5; DB 2; Length 1510;
Best Local Similarity 18.2%; Pred. No. 0.059;
Matches 160; Conservative 98; Mismatches 321; Indels 299;
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A; Residues: 1-527
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A;Description: Prediction of the coding sequences of unidentified human genes. VIII. The A;Reference number: Z14082
A;Reference number: Z14082
A;Accession: T00062
A;Accession: T00062
A;Accession: T00062
A;Accession: T10062
A;Accession: L1071
A;Coulcule type: mRNA
A;Residues: 1-1571
A;Coss-references: UNIPROT: O43161; EMBL: AB007894; NID: G2662148; PIDN: BAA23707.1; PID: G266Genetics:
A;Note: KIAA0434
                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                -SALRA 102
                                                                                                                                                                                                                                                103 SRGREBSDAP--TVQKSLS----YTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKL 155
                                                                                                                                                                                                                                                                                                                                        KAQERALDSAAP-----TFLLEQQLWGVELLPSSLQAGLVSHRELDSS 198
                                                                                                                                                                                                                                                                                                                                                    640 GGRDYPPLRGLGEHRDYLSDSELNQLRLQGCTTPAGQFVDFPATA---AAPATPSGPTAF 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHRRMRWLVFLOP----NOGODLPTLDQDNGYHSLEEEHNLLRMDPQHCTDN----- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAQAVSPAADRPEPTEKKPELVIQE-----VSQSPQ---GSSLFCELPVEKECEEDH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 TNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDW--GERPEDDGFD 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790 PRQTSLADLEQKVPTNYEVIASPVV---PMSSAPSETSYSGPAVSSGYEQGKVPEVPRAG 846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRGSVSQSPAPTYPSDSH----YTSLEQNVPRNYVMIDDISELTKDSTSTAPDSQRLBPL 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQPR-----PQPPAPQYSAGSGGPT---QNGF-------PAHQAPTYPGPSTY 734
                                                                                                                                                                                                                                                                                                  SSGPLSVQSLGNFKVVSYLLN-------PSYLDYLPQLGL--RCQSSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GGGQFVGFRTLTPESCYLSE-----DGC-HPQPLRAEMSATAWRRCPPLSTEGLPEI
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       Indels 179;
                                                                                                                                                                             Length 1571;
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                                                                                                                                                                          3.7%; Score 136.5; DB 2;
23.9%; Pred. No. 0.66;
tive 68; Mismatches 198;
                                                                                                                                                                                                                                LSOLLALLPSLFOKLLLWSOLSGGLIPTRWLD--FAASY
                                                                                                                                                                      Query Match
Best Local Similarity 23.9%;
Matches 140; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A;Residues: 1-782 <DBV>
A;Cross-references: UNIPROT:O16883; EMBL:AF022968; PIDN:AAB69883.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone C10F3
C;Genetics:
GB:chr_II; PIDN:AB66118.1; PID:g2315675; GSPDB:GN00020; CESP:F56D12.
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                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                  96 SYSA----LRASRGREESDAPTVQKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVLR 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --EEENENLKSKRRKSNIMRY--SPSLCDSDLSLNLHDKDSEDDEDRILNR---PSGCWS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDGCHPQPLR--AEMSATAWRRCPPLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTL--- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPNFFDETFRGVSPMNQKCW-----SAPDLEDIVFKTCNVLYNYDVIGGGKIPILREL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DQDN---GYHSLBEEHNLLRMDPQHC-----TDNPAQAVSPAADRPEPTEKK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 PELVIQEVSQS---PQGSSLFCELPVEKECEEDHŢNATDLSDRGESLPVSTRPVCSNKLI 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----APPTFNIGSDLEDNITEEEBBDDEED-----EEDVRKTEE---VW------ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 DYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDP 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PENATANFCWSDGVRRVHRSATFQINRYLDDDVTDGGT------VSPPLPRIT 414
                                                                                                                                                                                                                                                                                                                     90
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bacession: T33155
R;Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid C10F3.
A;Reference number: Z21127
A;A;Reference number: Z21127
                                                                                                                                                                                                                                                                                                151 LEVKLKAQE-----RALDSAAPTFLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVQSLGNPK-----VVSYLLNPSYLDYLPQLGLRCQSSAGGQQFVGFRTLTPESCYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 YKPQNFTAT-----IQTAA-----RIAPRDPSDSGTSWSGSCGVGSCQEGPLP---
                                                                                                                                                                                                          Gaps
                                                                                                                                              Query Match 3.6%; Score 135; DB 2; Length 527; Best Local Similarity 21.3%; Pred. No. 0.18; Matches 112; Conservative 57; Mismatches 178; Indels 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 VSRSAHSQLYNIGABETEDDADGDGDD---DDDVAENL---NENCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ETPDHSSGEEDDWEPSADEAENLKLWNSFCHS
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20.9%; Pred. No. 0.4;
tive 67; Mismatches 188;
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Best Local Similarity 20.9%;
Matches 108; Conservative
     A;Cross-references: G;Genetics:
A;Gene: F56D12.4
A;Map position: 2
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"Uppe-like (mycoplasma hyorhinis) lipoprotein [imported] - Mycoplasma pulmonis (strain UAE C; Species: Mycoplasma pulmonis C; Species: Mycoplasma pulmonis C; Species: Mycoplasma pulmonis C; Species: Mycoplasma pulmonis C; Statession: F90603 [S; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; A; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, W.; Samson, D.; Galisson, F.; Moszer, I.; Mycleic Acids Res. 29, 2145-2153, 2001
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    40,
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                                                                                              142
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                                                                                                                                                                                                                                                                        202 CDAGWLSDQTVRYPIQNPREACYGDMDGYPGVRNYGVVGPDDLYDVYCYAEDLNGELFLG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 GGGLPGVK-----TLFLFPNQ------TGFPSKQNRFNV-----YCFRDSAHPS 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AFSEASSPASDGLEAIVTVTEKLEELQLPQEAVESESRGAIY-SIPI-----TE 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSDSGTSWSGSCGVGSCQ---EGPLPETPDHS---SGEEDDWEPSADEAENLKLWNSPCH 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621
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                                                                                                                                                                                                                                          -----CHPOPLRAEMSA- 271
                                                                                                                                                                                                                                                                                                                                                                                    262 APPGKLITWEEARDYCLERGAQIASTGQLYAAWNGGLDRCSPGWLADGSVRYPIITPSQRC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                 --GLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPA--- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- QAVSPAADRPEP----TEKKPELVI-QEVSQSPQGSSLFCELPVEKECEEDHTNATD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 LSDRGESLPVSTRPVCSNKLIDYILGGAP-SDLEASSDS-----ESEDWGEEPEDDGFD 443
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                                                                             140 GGTPVAVLV---LRLEVKLKAQERALDSAAPTFLLEQQLWGVELLP--SSLQAGLVSHRE
                                                                                                                                              -GNFKVVSYLLNPSYLDYLPQLGLRCQ
                                                                                                                                                                                        143 DDSSDAVEVKVKGVVFLYREGSARYAFSFAGAQEACARIGARIATPEQL-YAAYLGGYEQ
                                                                                                                                                                                                                                                                                                                                       ----TAWR----RCP------PLSTE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 SEDPYNLINFKAPFQPSG-----KNWKGR-------QDSKASSEVTVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 LEDGPSLL -- PETWAPVGTREVETPSEEKSGRTVLTGTSVQAQPVLPTDSASRGGVAVAP
    Gape
    259;
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  Indele
                                                                                                                                                                                                                                             235 SSAG--GGQFVGFRTLTP-ESCYLSEDG-------
  Mismatches 217;
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Pred. No. 0.39;
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  63;
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    Matches 154; Conservative
                                                                                                                                              -195 LDSSSSGPLSVQSL
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A;Status: preliminary
A;Molecule type: DNA
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A;Genetic code: SGC3
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 0.1 Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: 849126; I55457
R;Seidenbecher, C.I.; Langnase, K.; Wax, H.; Seidel, B.; Garner, C.C.; Gundelfinger, B.D
R;Description: Molecular Library, June 1994
A;Description: Molecular cloning of a new member of the aggrecan/versican family of prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:PS5068; EMBL:X79881; NID:g509396; PIDN:CAA56255.1; PID:g5093 R;Seldenbecher, I.C.; Richter, K.; Rauch, U.; Fassler, R.; Garner, C.C.; Gundelfinger, B. Seldenbecher, I.C.; Gundelfinger, B. Seldenbecher, I.C.; Gundelfinger, B. A; Biol. Chem. 270, 27206-27212, 1995 A;Title: Brevican, a Chondroitin Sulfate Proteoglycan of Rat Brain, Occurs as Secreted A;Reference number: I55457; MUID:96070828; PMID:7592978
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C/Cross-references: EMBL:X79881; NID:g509396; PIDN:CAA56255.1; PID:g509397
C/Superfamily: Por an alternative aplice form, see PIR:A53908.
C/Superfamily: Aggreen; C-type lectin homology; complement factor H repeat homology; C/Seywords: alternative aplicing
F/49-138/Domain: immunoglobulin homology <IMM>
F/173-250/Domain: immunoglobulin homology <IMM>
F/271-350/Domain: link protein repeat homology <IMK1>
F/271-350/Domain: EGF homology <EGF>
F/66-657/Domain: EGF homology <EGF>
F/66-657/Domain: C-ype lectin homology <IMCA
FNSSGSSGEASEGESSGSEDQGSGN----YK---MIESIESSGEFSGSSGEGSGDTASS 610
                                                                                                             AGTLLSEVFVRPIAATQNKLSILRPILGTFMP---BQCGYLTNNAELKKHRIDATMDEEL 395
                                                                                                                                                                                                                                                                   ------VSQSPQGSSLFCELPVEKECEED------HTNATDLSDRGESL 398
                                                                                                                                                                                                                                                                                                                                                                ----SEILEHISEKSTEESSGSSGEMSGDGSDNEASGEGSGEYDASGSSGDNSGE 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLLNFKAPFQPSGKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPG---- 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661 ---GFGESSGSSGESIELRDSGEGSAEYDASGSSGD------NSGDFNSSGSSGEA 707
                                                                                                                                                                                                            KRMYAEKIAKEARDRTAQDEILANLVPLDENGVPLPRALPELKSIESPLDVSVKTLDQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S------CGVGSCQEGPLPETPDHSSGEE-DDWEPSADEAENLKLWNSFCHSEDPY
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                                                                          STEGLPEIHHR ----RMRWLVFLQPNQGQDLPTLDQDNGYHSLEEHNLLRMD-
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Pred. No. 0.47;
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A;Molecule type: mRNA
A;Residues: 1-883 <RES>
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brevican precursor - rat
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-883 <SEI>
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Qy 310 -LDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIOEVSGSPQG 368 Db 200 CLPPPRRQRPAETTAHLPPPRPQRPAETT-KVPEBIPPEVQ 254 Qy 369 SSLFCELPVEKECEBDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDS 428 Qy 429 ESEDWGEEP-EDDGFDSDGSL	nding protein - sea urchin (Strongylocentro Strongylocentrotus purpuratus (purple urch or 13028. Faspanola, M.; Klinzing, D.C.; Pfarr, K.; B 165, 73-85, 1994 ni 15, 73-85, 1994 ni 13028. Prepliminary; translated from GB/EMBL/DDBJ type: mRNA i 1-1560 «SOL» ferences: UNIPROT:Q26644; EMBL:L34680; NID:	Conservative S. C.
Matches 82; Conservative 59; Mismatches 133; Indels 125; Gaps 19;		Query Match Best Local Similarity 20.3%; Score 130; DB 2; Length 613; Best Local Similarity 20.3%; Pred. No. 0.49; Matches 139; Conservative 63; Mismatches 248; Indels 234; Gaps 31; Oy 17 GGWPRLPFLRRSHACSSEPPPSAGVAPIVSPGNAGLPERRTRYWTKLLSOLIALLPSLF 72 Op 7 GGWSHGLPLPPPPPAAQVAPIVSPGNAG

Db 468FSKLPRIPKIRRDGGNSTQDQAPASGQTVELPSACISRLTGREGPGQPG-RGRAD 521 Qy 428 SESEDWGEBFEDDGFDSGLSESDVEQDSEGLHUMNSFHSVDPYKPQNFTATIQTAARI 487	A. Molecule type: DNA A. Residues: 1.40 c.84L. A. Residues: 1.40 c.80 c.80 c.84L. A. Residues: 1.40 c.80 c.80 c.84L. A. Residues: 1.40 c.80 c.80 c.80 c.80 c.80 c.80 c.80 c.8
Db 1137VSEG	RESULT 12 To 1312 C. Cerminal domain-binding protein rA9 - rat C. Species: Rattue norvegicus (Norway rat) C. Species: T3142 R. Yuryer, A.; Patturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord A.7 Till: The C-reminal domain of the largest subunit of RNA polymerase II interacts with A.7 Till: The C-reminal domain of the largest subunit of RNA polymerase II interacts with A.7 Stetus: pre-liminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Nolecule typ

---- PLSVQSLGNFKVVSYLLNPSYLDYLPQLG

Gaps

Indels 144;

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A;Map position: 3
A;Introns: 683/1; 723/1; 769/2; 842/3; 877/1; 899/3; 908/1; 961/3; 1016/3; 1118/3; 1169/-
A;Note: T2J13.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSHAKFVEYRTAPSSEEGGNCFHYASRRVFQPQRIHHIDGSGFLKY-----NSDYITRKH 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEHNLLRMDPQHCTDNPAQAVSPAADR 347
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                                                                                                                                                                                                                                                                                        3.4%; Score 126; DB 2; Length 1229; Similarity 22.4%; Pred. No. 2.4; Conservative 63; Mismatches 209; Indels 144
A;Residues: 1-1229 <RIE>
A;Cross-references: UNIPROT:Q9SMV0; EMBL:AL132967
A;Experimental source: cultivar Columbia; BAC clone T2J13
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T4616
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23023
A;Accession: T46116
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein phosphatase 1 binding protein spinophilin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 09-Jul-2004
C;Accession: T03852
R;Allen, P.B.; Ouimet, C.C.; Greengard, P.
Proc. Natl. Acad. Sci. U.S.A. 94, 9956-9961, 1997
A;Title: Spinophilin, a novel protein phosphatasel binding protein localized to A;Reference number: Z15121; MUID:97420791; PMID:9275233
A;Accession: T03852
A;Accession: T03850
A;Accession: T03850
A;Accession: T03850
A;Accession: T03850
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ive 44; Mismatches 134; Indels
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                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
library, clone:C230033D15 product:hypothetical protein, full insert
sequence (Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-
length enriched library, clone:C530022L24 product:hypothetical
protein, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Cerebellum, and Spinal cord;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/64; TISSUE=Cerebellum, and Spinal cord;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=CS7BL/60; TISSUE-Cerebellum;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,
Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUB=Cerebellum, and Spinal cord; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKIN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Cerebellum, and Spinal cord; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; RIKEN FANTOM CONSORTIUM;
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Hukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayili Y., Itoh M., Kagawa T., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Saitoh H., Sakai C., Sakai K., Shiraki T., Sogabe Y., Tagami M., Saito R., Saitoh H., Sakai C., Sakai K., Shiraki T., Sogabe Y., Tagami M., Sasaki D., Shibata K., Shinagawa A., Takaku-Akahira S., Takeda Y., Tanaka T., Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tagawa A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tamaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Bubli, AK049028; BAC33517.1; -

BMBL; AK049028; BAC33517.1; -

BMBL; AK049028; BAC33517.1; -

BMBL; AK049028; EAC33517.1; -

BMBL; AK049028; EAC38517.1; -

BMBL; AK049028; EAC385
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Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saaski D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahiras S., Takeda Y., Tanaka T., Tonaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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697 AA; 77711 MW; E439B12615F33737 CRC64;
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                                                                                                                                                                                                                                                                                                    295 WLVFL-QPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP----B
                                                                                                                                                                                                                                                                                                                                           RIEFLQQASKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 ACSNKLIDYILGGASSDLETSSDPEGEDWDEBAEDDGFDSDSSLSDSDLEQDPEGLHLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540 EDDWESSADEAESLKTWNSFCNSDDYNPLNFKAPFQTSGENEKGCRDSETPSESIVAIS
                            LWGVELLPSSLOAGLVSHRELDSSSSGPLSVOSLGNFKVVSYLLNPSYLDYLPQLGLRCQ
                                                                                                                                                             SSAGGGQFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRMR
                                                                                                                                                                                                                                                                                                                                                                                                                                     350 PTEKKPELVIQEV----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ14744.
Homo sapiens (Human).
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"Generation and initial analysis of more than 15,000 full-length human
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                                   DNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRI
NSPCHSEDPYNLLNPKAPFQPSGKNWKGRQDSKASSEVTVAPSGHHTLLSCKAQLLESQE
                                                                                                                                       DNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFOKRI
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Director MGC Project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0652B0; AAH652B0.1; -.
SEQUENCE 713 AA; 79125 MW; 76C2DA38F9E76A85 CRC64;
                                                                                                                                                                                                                                                                                                           QETEVAIGYCLAFEHREKMFNRLRIESKDLLLYSNVKK 697
                                                                                                                                                                                                                                                                        QETEVALGYCLAFEHREKMFNRLRIESKDLLLYSNVKK 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein phosphatase 1, regulatory subunit 15B.
Name-PPPIRISB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 AA
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Matches
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Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizuno J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SALPERRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAPTFLLEQQ
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                                                                                                                                                                                                                                                                                                                                                                           Length 713;
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Genew; HGNC:14951; PPPIR15B.
SEQUENCE 713 AA; 79125 MW; 26C2D06144AAD25E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                           59.6%; Score 2213; DB 2; 164.8%; Pred. No. 2.6e-127; ive 55; Mismatches 174;
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Matches 454; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CSTREM(6): TISSUE-Brain),

STRAIN-CSTREM(6): STRAIN-CSTREM(6): TISSUE-Brain),

STRAIN-CSTREM(6): TISSUE-BRAIN-CSTREM(6): TISSUE-BRAIN
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GO; GO:0000164; C:protein phosphatase type 1 complex; IDA.

GO; GO:0004512; F:protein serine/threonine phosphatase activity; IDA.

GO; GO:00065182; F:translation regulator activity; IC.

GO; GO:0006983; P:ER-overload response; IDA.

GO; GO:0006464; P:response to diranslational initiation; IC.

GO; GO:0006379; P:response to hydrogen peroxide; IMA.

GO; GO:0006379; P:response to oxidative stress; IDA.
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                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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    Last sequence update)
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STRAIN=C57BL/6; TISSUE=Brain;
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05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                 musculus (Mouse)
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-Head;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashlzaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CSTBL/6J; TISSUE=Head;
THE FANTOM CONSORTIUM,
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
(60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunbate M., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii K., Kateunai T., Tashiro H., Itoh M., Sumi N., Ishii K., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateunico H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watahika M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 15 days embryo head CDNA, RIKEN full-length enriched
library, clone:D930040107 product:hypothetical protein, full insert
                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci IPukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
          EVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRPV 405
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR-GS7BL/6J; TISSUE-Head;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN PANTOM CORBORTLUM;
                                                                                                           376
                                                                                                                                       Created)
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                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23,
                                                                                                           PRELIMINARY;
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Name=Ppplr15b;
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Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nakamura M., Nakamura M., Nahi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shiragawa A., Shiraki T., Sogabe Y., Tanaka T., Takawa S., Takada Y., Muramateu M., Hayashiaki Y., Rubi Y., Takada Y., Muramateu M., Hayashiaki Y., Takada Y., Takada Y., Takada Y., Takada Y., Takada Y., Takada Y., Yanaka Y., Takada Y., Takada Y., Takada Y., Yanaka Y., Takada Y., Yanaka Y., Takada Y., Yanaka Yanak
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The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo
Han M., Wiemann S.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
NON TER 376 376
SEQUENCE 376 AA, 41949 MW, 972525D3D472C8F8 CRC64,
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25-OCT-2004 (TrEMBLrel. 28, Last sequence up
25-OCT-2004 (TrEMBLrel. 28, Last annotation of thypothetical protein DKFZp6661186 (Fragment)
Name=DKFZp6661186;
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3 360
1 398
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71840 MW; 5
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Best Local Similarity 21.5%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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657 AA;
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SEQUENCE FROM N.A.
                                                                                                                                               LRIE 686
                                                                                                                                                                                                        LKYE 155
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                                                                                                                                                                                                                                                                                                                                                     M116 MOUSE
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DE M116 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                           358 VIOEV----SOSPOGSSLFCELPVEXECEEDHTNATDLSDRGESLPVSTRPVCSNKLID 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPY 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 GKNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKR 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLID 121
                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                       2 SKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 NPONFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEEDDWESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 KPQNFTATIQTAARIAPRDPSDSGTSWSGSCGV-GSCQEGPLPETPDHSSGEEDDWEPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEAENLYCLWNSFCHSEDPYNLINPKAPFOPSGKNWKGRODSKASSEVTVAFSGHHTLLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRKGPWEEFAR
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Pubmed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
The genome of canarypox virus.";
J. Virol. 78:353-366(2004).
EMBL; AY318871; AAR83577.1; -.
SEQUENCE 158 AA; 18892 MW; FEB7CDF3E796421C CRC64;
                                                                                                                                                                                                                                   10;
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                                                                                                                                                                             Length 407;
                                                                                                                                                                       Query Match 37.5%; Score 1392; DB 2; Length 4 Best Local Similarity 69.5%; Pred. No. 2.7e-77; Matches 273; Conservative 27; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Indels
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                                                                                                                                                                                                                                                                                            302 NQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AL033746; CAH56240.1; -. Hypothetical protein.
                                                                                                                 F5AFFAEF48BB3704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CNPV231 MyD116-like domain protein.
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34.2%; Pred. No. 3.8e-08;
iive 19; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGCRPQKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                                                                                                 407 AA; 45218 MW;
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Best Local Similarity
Matches 63; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avipoxvirus.
NCBI_TaxID=44088;
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SEQUENCE
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                                        93 SVVTFSETIIEYHVP-YEDRKGPWEEIARDRYRFEKRIKETAEIIEFCLSENHRRNIKTH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQQLWGVELLPS-SLQAGLVSHRELD-SSSSGPLSVQSLG-----NFKVVSY---LLN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 PSYLDYLPQLGLRCQSSAGGGOFVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRCPP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 YTAAGLFAKTRVVSTLALARG----GTPVAVLVLRLEVKLKAQERAL---DSAAPTFLL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 IEAAALLTPTPVSGNL-LPHGETEESGSP------EQSQAAQRLCLVEAESSPP--- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90251472; PubMed=2339071;
Lord K.A., Hoffman-Liebermann B., Liebermann D.A.;
"Sequence of MyD116 cDNA: a novel myeloid differentiation primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%; Score 204; DB 1; Length 657;
21.5%; Pred. No. 0.00035;
tive 86; Mismatches 290; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
Myeloid differentiation primary response protein MyDll6.
Name—Mydll6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 (incomplete).
9B217001019C38A7 CRC64;
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Nucleic Acids Res. 18:2823-2823(1990).
-!- INDUCTION: By interleukin-6.
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Strausberg
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                                                                      255 AHRAGQGHPCRNAEAEEGGPETTF--VCTGNAFLKAWVYRPGEDTEEEDNSDSDSAEEDT 312
                                                                                                                         DTEENSDLDS--AEEDTAQTGATPHT-SAFLKAWVYRPGEDTEENSDLDSAEEDTAQT 429
                                                                                                                                                                                                                                                                        556 KAPFQPS----GKNWKGRQDSKASSEVTVAFSGHH------TLLSCKAQLLES-- 598
                                                                                                                                                                                                                                                                                       LSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQ 339
                                                     AVSPAADRP----EPTEKKPELVIQEVSQSPQGSSLFCELPVEKECEEDHTNATDLSDRG 395
                                                                                                                                                              EPEDDGFDSDGSLSESDVEQDSEGLHLWNSFHSVDPYKPQNFTATIQTAARIAPRDPSDS 495
                          200 TPVPFLGBAEHQATE----EKGTENKADPSNSPSSGSHSRAWEY-YSREKPKOEGEAKVE 254
                                                                                                                                                                                                                                 | : | : : | : | | GATPHTSPFLKAWVYRPGEDTEDDTEEEEDSENVAPGDSETADSSQSPC-----
                                                                                                                                                                                                                   GTSWSGSCGVGSCQEGPLPETPDHSSGEEDDWEPSADEAENLKLWNSFCHSEDPYNLLNF
                                                                                                                                                                                                                                                                                                                            --OEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSUE-Heart;
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                        ESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESED-
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                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       311 DQDNGYHSLEEEH--NLLRMDPQHC--TDNPAQAV-------SPAADR 347
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                                                                                                                                                                                                                                                                                                                                                                                  LRETEGNGTPEWSKAAQRLCLDVEAQSSPPKTWGLSDIDEHNGK-----PGQD--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GLREQEVEHTAGLPTLQPLHLQGADKKVGEVVAREEGVSELAYPTSHWEGGPAEDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTEKKPELVIQEVSQSP---QGSSLFCELPVEKECEED-------HINATDLS 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 LESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                             Length 578;
                                                                                                                                                                Indels
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072513; AAH72513.1; --
SEQUENCE 578 AA; 63583 MW; D9387CA71923345F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 22:3827-3832(2003).
EMBL; AY128642; AAM77795.1; -.
SEQUENCE 578 AA; 63569 MW; 923EC49921COBC61 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein phosphatase regulatory subunit 15A.
                                                                                                          5.1%; Score 190.5; DB 2;
22.8%; Pred. No. 0.002;
iive 58; Mismatches 214;
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                                                                                                                                                                  Conservative
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                                                                                                                                         Similarity
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Matches 131;
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                                                                                                                                                           20 YLLSP-LMGFLSRAWSRLRGPEVSRAWLAETVAGANQIBADALLTPPP--VSENHL---P
                                                                                                                                                                                                                                                                                                          74 LRETEGNGTPEWSKAAQRLCLDVEAQSSPPKTWGLSDIDEHNGK-----PGQD----
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TISSUB=Brain;
MEDLINE=2138825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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MEDLINE=97298078; PubMed=9153226; DOI=10.1074/jbc.272.21.13731;
HOllander M.C., Zhan Q., Bae I., Fornace A.J. Jr.;
"Mammallan GADD34, an apoptosis- and DNA damage-inducible gene.";
J. Biol. Chem. 272:13731-13737(1997).
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                                                            171;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Apoptosis associated protein (Protein phosphatase 1, regulatory
      Length 578;
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Catarrhini; Hominidae; Homo
                                                               Indels
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5.1%; Score 189.5; DB 2;
22.8%; Pred. No. 0.0023;
iive 58; Mismatches 214;
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Name=GADD34; Synonyms=PPP1R15A;
Homo sapiens (Human).
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Mammalla; Eutheria; Primates;
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                                                               Conservative
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                            Best Local Similarity
Matches 131; Conserv
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soarsa M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boaks S.A., McKernan P.J., McKernan R.J., Malke J.A., Gunarane P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia R.A., Sodinges S., Sanchez A.,

R. Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

M. Rizzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

R. Marra M.A., Smailus D.E., Schnerch A., Schein J.E.,

R. Menting M. Bornara M.A.,

Jones S.J., Marra M.A.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VEAGLEGEAR------TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KE-----EKAHKETGKGEAA-----PGPQSSAP-----AQRPQLKSWWCQPSDEEE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEVKALGAAEKDGEAECPPCIPPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA---
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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EMBL; BC003067; AAH03067.1; -.
GGROW; HGWC:14375; PPPDR15A.
GO; GO:0006915; P:apoptosis; TAS.
GO; GO:0007056; P:cell cycle arrest; TAS.
GO; GO:00070574; P:response to DNA damage stimulus; TAS.
SEQUENCE 674 AA; 73477 MW; B257AA17456D1403 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSPVMGLLSR-----AWSRLR-GLGPLEPWLVEAVKGAAL
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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21.5%; Pred. No. 0.0028;
tive 74; Mismatches 269;
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60 LISQLIALIPSIFQKILIWSQLSGGLIPTR-WLDFAASYSALRASRGREESDAPTVQKSL 118
                                                                                           321 EEHNILIRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678
--TPLA--IPHTPWGRRPGEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVKPLGAAEKDGEAECPPCIPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 GSDEEEGEAEASSSTPATGVFLKSW-----VYOPGEDTEEEEDEDSDTGSAEDEREAE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPYNLLNFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 604 PGCGLGEA------TAGER----------------YTHIKRK 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----WGEAEPCPFRVAIYVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHDPDPETPLKAR 554
                                                                                                                                                                                                            ------WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE
                                                                                                                                                                                                                                                                                                                          211 LSPGSKPSTWVSCPGEBENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGERSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                           :| : | : | : | | | | | KE-----AQRPQLKSWWCQPSDEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ-----TAARIAPRDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 DSGTSWSGSCGVGSCQEGPLPETPDH-----SSGEEDDWEPSADEAENLKLWNSFCHSE
                                                                                                                                                                       --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 TSASTPPASAFLKAWVYRPGEDTEEEEDEDVDSEDKEDDSEAALGEAES------
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21.3%; Pred. No. 0.012;
Antive 74; Mismatches 270; Indels 227; Gaps
                                                      FILEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL--
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR457259; CAG33540.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73523 MW; 88A2EE1AF5EDE678 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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   --VEAGLEGEAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Matches 155;
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SEQUENCE FROM N.A.

OCE T., Suzuki Y. V. Niehkawa T., Otsuki T., Sugiyama T., Irie R.,

A CET T., Suzuki Y. V. Niehkawa T., Otsuki T., Sugiyama T., Irie R.,

A CET T., Suzuki Y. Niehkawa T., Otsuki T., Kimura K., Makita H.,

Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

A Mamancto J., Saitor K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

A Murakami K., Yasuda T., Iwayanagi T., Wagatsum M., Shiratori A.,

Sudo H., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Dek K., Kanihara K., Yatuki T., Yasashita H., Murakawa M., Yamazaki M.,

A Dek K., Kamihara K., Yatuki T., Yasashita H., Murakawa M., Yamazaki M.,

A Takai H., Kimata M., Matanabe S., Yosida M., Hotuta T., Kusano J.,

Kanachori K., Takiguchi S., Watanabe S., Yosida M., Hotura T., Kusano J.,

A Togiya S., Komai F., Hara R., Takeuchi K., Arita W., Imose N.,

Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

Noriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Sazuki O.,

Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

A Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

A Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

A Namazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

A Nahagawa S., Senoh A., Mizoguchi H., Taro M., Ohmori Y.,

A Nahagawa S., Senoh Y., Noguchi S., Itoh T., Shigeta K., Senba T.,

A Natumura K., Nakajima Y., Matanabe M., Komateu T.,

Matsushima Sugano J., Satoh T., Shigeta K., Sabaki M.,

A Togashi T., Oyama M., Hata H., Watanabe M., Komateu T.,

Matsushima Sugano J., Satoh T., Shigeta K., Sabaki M.,

A Nakai K., Yada T., Noguchi H., Matanabe M., Komateu T.,

Matsushima Sugano J., Satoh T., Shara J., Sagaki M.,

A Nakai K., Yada T., Noguchi H., Matanabe M., Kakuhi R., Nakai K., Nakai K., Nakai K., Nakai K., Nakai K., Nakai M., Nakai M., Nakai K., Nakai M., Nakai 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAQERALDSAAP-----T 168
                                                                                                                                               KVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678
                                                                                                                                                                                    ----WGEAEPCPFRVAIYVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHDPDPETPLKAR 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSQLLALLPSLFQKLLLWSQLSGGLIPTR-WLDFAASYSALRASRGREESDAPTVQKSL
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL; AK001361; BAA91649.1; -.
SEQUENCE 674 AA; 73363 MW; 8F988E873B29CBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10499.
Homo sapiens (Human).
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                                 PGCGLGEA------LAGER-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       615 AWARLR 620
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EMBL; L28147; AAA36983.1; -.
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                         PIR; A56535;
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                                           SEQUENCE
                                                                                     Query Match
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                                                                                     --VEAGLEGEAR-----TPLA--IPHTPWGRRPEEEAEDSGGPGEDRETLGLKT 100
                                                                                                                                                                                                                                                                   GSDKNP--GEEKAEEEGVAEEEGVNKFSYPPSHRECCPAVEEEDDEEAVKKEAHRTSTSA 210
                                                                                                                                                                                                                                                                                                            -----WRRCP----PLSTEGLPEIHHRRMRWLVFLQPNQGQDLPTLDQDNGYHSLE 320
                                                                                                                                                                                                                                                                                                                                                                                                    EEHNLLRMDPQHCTDNPAQAVSPAADRPEPTEKKPELVIQEVSQSPQGSSLFCELPVEKE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEEDHTNATDLSDRGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDD 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPH-----PSHPDQRAHFRGWGYRPGKETEEE--------EAAED-- 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVTFLEEVTEYYIS----GDEDRKGPWEEFARDGCRFQKRIQETEVAIGYCLAFEHREK 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPDSDGSLSESDVEQDSEGLHL--WNSFHSVDPYKPQNFTATIQ-----TAARIAPRDPS 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 PGCGLGEA-----YTHIKRK 623
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                                                                                                                                 FLLEQQLWGVELLPSSLQAGLVSHRELDSSSSGPLSVQSLGNFKVVSYLLNPSYL----
                                                                                                                                                                           SSSLPEAWG--LLDD--DDGMYGEREATSVPRGQGSQFADGQ----RAPLSPSLLIRTLQ
                                                                                                                                                                                                                         --DYLPQLGLRCQSSAGGGQFVGFRTLT----PESCYLSEDGCHPQPLRAEMSATA---
                                                                                                                                                                                                                                                                                                                                                           LSPGSKPSTWVSCPGEEENQATEDKRTERSKGARKTSVSPRSSGSDPRSWEYRSGEASEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVKALGAAEKDGEAECPPCIPPPSAFLKAWVYWPG---EDTEEEEDEEE----DEDSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSGTSWSGSCGVGSCQEGPLPETPDH----SSGEEDDWEPSADEAENLKLWNSFCHSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPYNLLINFKAPFQPSG----KNWKGRQDSKASSEVTVAFSGHHTLLSCKAQLLESQEDNC
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01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-UNOV-2003 (TYEMBLrel. 24, Last annotation update)
01-UND-2003 (TYEMBLrel. 24, Last annotation update)
Gadd34 protein.
Name=Gadd34;
Cricerulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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MEDLINES-94187707; PubMed=8139541;
Zhan Q., Lord K.A., Alamo I.Jr. ., Hollander M.C., Carrier F.,
Kohn K.W., Hoffman B., Liebermann D.A., Fornace A.J.Jr. .;
Kohn K.W., Moffman B., Liebermann D.A., Fornace A.J.Jr. .;
"The gadd and MyD genes define a novel set of mammalian genes acidic proteins that synergistically suppress cell growth.";
MOI. Cell. Biol. 14:2361-2371(1994).
                                           SYTAAGLFAKTRVVSTLALARGGTPVAVLVLRLEVKLKAOERALDSAAP-
LLSPVMGLLSR-----TWSRLR-GLGPLEPWLVEAVKGAAL-
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SEQUENCE FROM N.A.
MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
MCBI TaxD=7227,
                                                                                           Length 590;
                       B3D879BDACBAE6D6 CRC64;
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                                                                                        4.6%; Score 171.5; DB 2;
18.1%; Pred. No. 0.03;
tive 68; Mismatches 198;
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590 AA; 64527 MW;
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01-MAY-2000 (TrEMBLrel. 13,
25-OCT-2004 (TrEMBLrel. 28,
CG6296-PA (LP07116p).
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Buckok J., Broketain P., Botcher R., Charler B., Botcher M., Buck J., Broketain P., Botcher R., Chaleu E., Center A., Chandra I., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Charler B., Dandey S., Dahlke C., Davenport L.B., Davies P., Charler B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.B., Downes M., Digan-Rocha S., Pleischmann M., Robert C., Cabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Anderin M., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Anderin M., Kalush F., Karpen G.H., Ke Z., Kannison J.R., Ketchum K.A., Mamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., Marteil B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Moshrefi B., McIntosh T.C., McLeod M.P., McPherson D., Melson D.R., Nelson K.A., Nixon X., Nusskern D.R., Pacleb J.M., Nelson K.A., Nixon X., Nusskern D.R., Pacleb J.M., Resen M.G., Shener E., Shen H., Spier E., Spradling A.C., Stapleton M., Skrong R., Sun E., Syradling A.C., Stapleton M., Skrong R., Sun E., Syradling A.C., Stapleton M., Skrong R., Sun E., Syradling A.C., Stan M., Zhong W., Zhou S., Yao Q.A., Ye J., Yen R., Mars S., Wasserman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Wooddag-T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Weisser B.W., Rubin G.M., Venter J.C.; R., Mars R.A., Myer E.W., Rubin G.M., Venter J.C.; Stan K., Mars B.N., Shun S., Zhon K., Smith H.O., Schele R.M., Myer E.W., Rubin G.M., Venter J.C.; Shan K., Mars B.N., Shun S., Zaveri J.St., Shon S., Shun 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2145065; PubMed=12537568; MEDLINE=2145065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotqun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
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MEDINBE-21426070; PubMed=12537573;
MEDINNBE-21426070; PubMed=12537573;
Maminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Raminker J.S., Perise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426069; PubMed=12537572;
Mista B., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Betteencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J. Kusso S., Schroder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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STRAIN=Berkeley;
Stapleton M., Broketein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dreenek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
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Pfam; PP00151; Lipase; 1.
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Flyames, Figures, 1970; CG6296.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0006629; P:lipid metabolism; IEA.

InterPro; IPR00234; Dol/Ves_allerg.

InterPro; IPR00374; Lipase.

InterPro; IPR00379; Ser_estrs.
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Search completed: September 16, 2005, 10:46:02 Job time : 75.2452 secs

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Submitted (SEP-2002)

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Run ξ

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Abk28397 DNA trans
Abk1265 Signal tr
Abl7020 Chemicall
Aa861175 Human Obe
Abl68807 Human Obe
Abl68807 Kidney ca
Ada1381 Human int
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Ab138451 Human cOl
Aac29803 Human sec
Abx44494 cDNA enco
Abx52167 Bovine ES
Aac6938 Human sec
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                                                                                                                                                                                                Oxidative stress; neuronal ischaemia; heart ischaemia; renal damage; autoimmune disease; neurodegenerative disorder; therapy; GADD34-like; GADD34L; eIF2alpha-specific regulatory subunit; phosphatase; human; gene;
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iive 0; Mismatches
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                                                                                  CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGAGGCCGTGGGGGGGACT
                                                                                                      CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGAGGCCGTGGGGGGAGACT
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TTCCTACCTGGACTGCTTTCCTAGGCTAGAAGTCAGCTATCAGAACAGTGATGGAAATAG	1141 CGAGGTAGTCGGCTTCCAGACACTAACCCCAGAGAGCAGCTGCCTGAGAGAGCACCATTG 1200 1201 TCATCCCCAGCGCTGAGTGCAGAACTCATTCGGGCTCGTGGCAGGGATGTCCACCTCT 1260 1201 TCATCCCAGCGCTGAGTGCAGAACTCATTCGGGCCTCGTGGCAGGGATGTCCACCTCT 1260	TTCTACGGAAGGCCTACCAGAATTCACCATCTTCGCATGAAACGGCTGGAATTCCTTCA TTCTACGGAAGGCCTACCAGAAATTCACCATCTTCGCATGAAACGGCTGGAATTCCTTCA TTCTACGGAAGGCTACCAGAAATTCACCATCTTCGCATGAAACGGCTTGGAATTCCTTCA	AGCCT AGCCT	1381 GGAGGAGGAACACGCTTCTCCGGATGGATCCAAACACTGCAGAGATAACCCAACACA 1440	GTTTGTTCCTGCTGCAGACATTCCTGGAACACCCAGGAATCCACTGAAGAAAAAT 	AGANTATTAACTACAGAGGTTCCACTTCCTTTCGAAGAGAGACCCCTTCTGAGGGCTG 	TCCATCTAGTGAGATACCTATGGAAAAGGAGCCTGGAGAGGCCGAATAAGTGTAGTTGA 		GATAGATTATATTTTGGGAGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCGAGAAGGGGAAGATTTTTGGAAGGAGGTGCATCAGTGACTGGAAACAAGTTCTGATCCAGAAGA	TGAGGATTGGGATGAGGAGGCTGAGGATGATGGTTTTGATAGTGATAGCTCACTGTCAGA	1801 CTCAGACCTTGAACAAGACCCTGAAGGGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGA 1860 	1861 TCCTTATAATCCCCAGAACTTTACAGCAACAATTCAGACTGCCAGAATTGTTCCTGA 1920 	1921 AGAGCCTTCTGATTCAGAAGGATTTGTCTGGCAAGTCTGATCTAGAGAATTCCTCCCA 1980 	1981 GTCTGGAAGCCTTCCTGAGACCCCTGAGCATAGTTCTGGGGAGGAGGAGGACGAGTCC 2040 	2041 TAGTGCAGATGAAGCAGAGAGTCTCAAACTGTGGAACTCATTCTGTAATTCTGATGACCC 2100 	2101 CTACAACCCTTTAAATTTTTAAGGCTCCTTTTCAAACATCAGGGGAAAATGAGAAAGGCTG 2160

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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotides, or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a polynucleotide which comprises a 5'-end
sequence, where the
coligonucleotide which comprises as 1's nucleotides and the combination of
the 5'-end sequence[3'-end sequence is selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
capen therapy. The primers are useful for synthesising polynucleotides,
capencification and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
contains and/or diagnosis of the abnormality of the full-length
contains and/or diagnosis of the abnormality of the full-length
contains and/or diagnosis of the abnormality of the proteins encoded
AAH13613 to AAH13613 to AAH13613 to AAH13613 represent
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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Otsuki T;
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A, Nagai K,
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Sugiyama T, Wakamatsu A,
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99JP-00300253.
2000JP-00118776.
2000JP-00183767.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                   28-JUL-2000;
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240 240 120 180 120 180 300 300 GCCACCGCTGGGCAAGGCCGAGACTCTGTAGGCTTCCTCCGAATCCCGTCGACCTCCAGC 360 9 9 1 ATTITIGGCTTCGCTTCCACCGCACCAGCCGGCCTACCCAGTCCTTCCGGTATCGCGTTG crcaggggcrrrrcaacccrcrgrcagrcggaaaaccarcgccgaggccgrgggggacr CCTATCCATGGTGTTGAAGCGTCGAGCCGACTAGGGAACCTCCTTCCCCGCCAGGATGGA CCGCATTCGCTGCCCTCTGTGGCTTTTCTGCTGGCTCGAAGATCGGCCTGGAGCAGCGAC CGCATTCGCTGCCTCTGTGGCTTTTCTGCTGGCTCGAAGATCGGCCTGGAGCAAGAC Gaps ö Score 2934; DB 4; Length 2942; Pred. No. 0; 0; Mismatches 5; Indels 0; Query Match 99.7%; Best Local Similarity 99.8%; Matches 2937; Conservative 19 61 121 121 181 181 241 301

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1140 1200 1200 1260 1320 1380 1380 1020 TTCTACGGAAGGCCTACCAGAAATTCACCATCTTCGCATGAAACGGCTGGAATTCCTTCA 1320 GGAGGAGGAACACAGCCTTCTCCGGATGGATCCAAAACACTGCAGAGATAACCCAACACA 1440 TICCTACCIGGACTGCTTTCCTAGGCTAGAAGTCAGCTATCAGAACAGTGATGGAAATAG 1140 360 420 420 480 540 480 540 9 9 99 999 720 720 780 780 840 840 900 960 960 841 AGGGATCCACTGGCAATACTCGCCCCAGACCTAAAATTGGAGCTTAAGGCCAAGGGAAG 900 GCACCGCTGGGCAAGGCCGAGACTCTGTAGGCTTCCTCCGGAATCCCGTCGACCTCCAGC TTCCTACCTGGACTGCTTTCCCAGGCTAGAAGTCAGCTATCAGAACAGTGATGGAAATAG CGAGGTAGTCGGCTTCCAGACACTAACCCCAGAGAGCAGCTGCCTGAGAGGAGGACATTG cecricadecececececeracereadadacrereadadadadadadadadedeegade CCCTCGGCGATCGCAAGCAGGCTCTTCTAAGTTCCCGACGCCTCTTGGCCCCGGAAAACTC CGGGAACCCCCACACTGCTTTCCTCTGCCCAGCCCCGAGACTCGGGTCAGTTACTGGACGAA CCAACTTTTCGGTGGAATGTTTCCGACCAGATGGCTAGATTTTTGCTGGAGTCTACAGCGC CCTGAGAGCCCTGAAGGGACGGGAGAACCAGCCGCCCCCACAGGGGAAAATCTTTGAG ACAGGCTAACAAGGGGCAAGATTTACCCACCCCTGACCAGGATAATGGCTACCACAGCCT CGCTGAGCGCCGCGCCCTACCTGAGAGACTGTCAAGAAAAAGGAGATGGAGCCGGGGAC <u> AGGCGGGATCGCGGAAACGGCCTTGGCCCTCGGGCGGCTTCCGGTTCTGGCCACCCTTTTT</u> CCCTCGGCGATCGCAAGCAGGCTCTTCTAAGTTCCCGACGCCTCTTGGCCCCGGAAAACTC ACTGCTCTCCCAGCTCCTTGCGCCGCTCCCCGGATTGCTTCAGAAGGTGCTAATTTGGAG CCAACTITICGGTGGAATGITICCGACCAGATGGCTAGATTTTGCTGGAGTCTACAGGGC GGGGATCCACTGGCAATACTCGCCCCCAGACCTAAAATTGGAGCTTAAGGCCAAGGGAAG GTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTGGCCTC 1201 TCATCCCCAGCCGCTGAGTGCAGAACTCATTCCGGCCTCGTGGCAGGGATGTCCACCTCT CGGGAACCCCACACTGCTTTCCTCTGCCCAGCCCGAGACTCGGGTCAGTTACTGGACGAA TGCTTTGGACCCTGCAGCATTTTCTCTTAGAGCAGCAGCTGTGGGGAGTGGAGCT GTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTCGCCCTC TTCTACGGAAGGCCTACCAGAAATTCACCATCTTCGCATGAAACGGCTGGAATTCCTTCA 961 1081 361 361 421 421 481 481 541 541 601 601 661 721 721 781 781 841 901 901 961 1021 1021 1081 1141 1141 1201 1261 1261 1321 1321 1381 301 661 ઠે 셤 셤 셤 a g 셤 셤 셤 ð à 8 ઠે 셤 ⋧ à 셤 à ઠે Š 셤 ઠે 셤 ò 셤 δ g ò g 원 à 셤 ð ò ð

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Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
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2881 ACAATACTTATAGGGCTTAAAGCCCATTTTCATTTCTAATCTAAATTATGTGTGCCTATC
                                                 TACCICITACCIGAGAGGIGICITITAAAACAAAICITGGCAGCIGICCITIGACAITI
                                                                                                                                                                      ACTCAGAAACATTCAGGTTTGAAGCCAGCCCTGATAATGAAGGATGAACTAGTGTGATTT
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                                                                                TACCTCTTACCTGAGAGGTGTCTTTTAAAAACAAATCTTGGCAGCTGTCCTTTGACATTT
                                                                                                                                                   Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointeetinal; nephrotropic; antilnfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; se.
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GGAGGAGGAACACCCTTCTCCGGATGGATCCAAAACACTGCAGAGATAACCCAACACA 1440
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                                                 GTTTGTTCCTGCTGCTGGAGACATTCCTGGAAACACCCCAGGAATCCACTGAAGAAAAAT
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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have evectatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, immune system cardiovascular disorders, AAC9874 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5468;
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Matches 1964; Conservative
                                                                                                                                                                                                          WPI; 2004-552556/53
P-PSDB; ADQ88460.
ບ່
                                                                                                          Jousse C;
JOUSSE
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1831 TCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAGCAAC		2191 2198 2251 2258 2318	2371 TGAGGATCGCAAAGCACCATGGGAAGAATTTGCAAGGGATGCATGC	2498 GTTTAATAGACTGAGGATCGAAGGACTTACTGTTGTACAGGAATGTTAAGA 2553 2551 TGGCAGCCTGTAGTCTAGCTACCTCCTTACCTGAGAGGTGTCTTTTAAAA 2610 2554 AGTGA-ACAGCCTGCAACCGTGCCCACTCTGTCTCTTACTTGAGA-GTTTCCTTAAAA 2611 2611 ACAAATCTTGGCAGCTGTCCTTTGACATTTTTTTTTTAGAGAAATGTAACTTGGATCT 2670 2612 AGAAACCTGGCAGCTGTCCTTTGACATTTTTTTTTTTAGAGAAATGTAACTTGGATCT 2670 2612 AGAAACCTGGCAGCTGTCCTTGAACAGTTTTTTTTAAAGAAACAACTTGAAGCCAGCC	2672 CAGTTTGATTATTTTTGGGTAATGTGTCTCATTAGAAACACCAACT 2717 2731 CTGATAATGAAGGATGAACTAGTGTGATTTCTAATCCTCCTTTTTTGATTTAGTTGGGT 2790 2731 CTGATAATGAAGAATCTCTTATCTGTAATCCTCTTTTTCTATTTAGTTGGAT 2771 2791 GTGCTTTT 2798 [RESULT 5 AAH99389 ID AAH99389 standard; cDNA; 883 BP.
CTAGATTTTGCCGCAGGTTACAGGCCCTGAGAGGTCTTCGAGAGGACGGAGGATCTGAC GCCCCCACAGCGCAGAAATCTTTGAGTT-CGCTGCAGCTCGACTCCTCAGACCCCTC GL [912 - CTGGAAGTTAAACTCAAGGCCCAGGAAAGAGTTTAGACTCTGCAGGCCCCACTTTCCT 970	TITICAAGGIAGTITCCTAITCTCTGAACCCTTCCTGACTTGACT	CACCA 1330 CCCAC 1350 CCCAC 1387 ATGA 1410 ATGA 1447	cccachacattecacharaacccachagecgeteccctgctgcachachagecc aaacacccaggaatccactgaagaaaaatagaattattaactacagaggctccctgctgc aaacacccaggaatccactgaagaaaaaaccagaattggtattcacttgc TTGGaagaggcccttctgaggagtccattagtgaattcagaagaattgc TTGGaagaggcccttctgagggtccattagtggaatactagaaagaa		1771 TGGTTTTGATAGTGATAGCTCACTCAGACCTTGAACAAGACCTGAAGGGCT 1830 RES

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Gape 9

14; Indels

Mismatches

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Conservative

Matches 863;

AAH99389;

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AMM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinitlanmantic; antirheumatic; chey are expressed in, such as: antinitlanmantic; cardiovascular in such as: antinitlanmantic; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antidabetic; osteopathic; dermatological; antialteric; vulnerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocycopaenia, wounds, burns, ulcers, anaemia, platelet disorders, thrombocycopaenia, wounds, burns, ulcers, animitie, asthma, dispetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and neurological disorders
                                                                                                                                                                               antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-Hrv; fungicide; antimutagen; cardiavascular; antianaemic; anaemia; anti-Hrv; fungicide; antimutagen; cardiavascular; antianaemic; anaemia; antiagregant; haemostatic; untimatry; antidiabetic; cytostatic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; immunostimulant; gene therapy; antiaense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaemia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                                                                                                             cancer; ulcer; HIV infection; human immunodeficiency virus;
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                                                                                                                Human protein encoding cDNA sequence SEQ ID NO:224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 398; 1217pp; English.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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Score 828.6; DB 4; Length 883; Pred. No. 5.4e-236;

28.2%;

Best Local Similarity

Query Match

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                          1 AGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGATTGGGATGAGGAAGCTGAGGAT
                                                   GATGGTTTTGATAGTGATAGCTCACTGTCAGACTCAGACCTTGAACAAGACCCTGAAGG
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                                                                        GCCACCGCTGGGCAAGGCCGAGACTCTGTAGGCTTCCTCCGAATCCCGTCGACCTCCAGC
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                                              CCGCATTCGCTGCCCTCTGTGGCTTTTTCTGCTGGAGAGATCGGCCTGGAGCAGCGAC
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Sugiyama T, Wakamatsu A, Nagai K,
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11-JAN-2000; 2000JP-00118776.
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09-JUN-2000;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

[a) an oligo-dr primer and an oligonucleotide comprises one of the 5602 complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence in selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13612 to AAH13612 represent human amino acid sequences; and AAH13612 represent considered and the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTATCCATGGTGTTGAAGCGTCGAGCCGACTAGGGAACCTCCTTCCCCGCCAGGATGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTCGCATCAGTCGCCGCCTATTGCGCGGGCTGTTCTTCCCTGTGTTCTGCCGCCGCTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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    Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Arririedecricecriceaccedecedecedeceraceagrecricegrarecegric
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                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3458; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 772 BP; 134 A; 256 C; 217 G; 161 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Y
Otsuki T;
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Pred. No. 5.7e-209;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                           29-JUL-1999; 99JP-00248036.
27-A02-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00188767.
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98.8%;
                                                                                                                                                                                 28-JUL-2000; 2000EP-00116126
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Best Local Similarity 98.6
Matches 752; Conservative
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Sugiyama T,
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                                                 Homo sapiens
                                                                                           EP1074617-A2
                                                                                                                                     07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1' and sequence complementary to a
polynucleotide which comprises a 1' and sequence of polynucleotide which comprises a 1' and sequence of sequence oligonucleotide comprises a 1' and sequence of polynucleotide which comprises a 1' and sequence of sequence oligonucleotide which comprises a 1' and sequence of sequence oligonucleotide which comprises a 1' and sequence of sequence oligonucleotides and the combination of
the 5' end sequence 1's end sequence in antisense therapy and in
gene therapy. The primers sets can be used in antisense therapy and in
gene therapy. The primers are useful for synthesising polynucleotides,
centection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers are also useful for the
cDNAs easily without any specialised methods. AAH13612 to AAH13622 represent
center of the full-length are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2400 TTGCAAGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAACAGAAGATGCTATTGGAT 2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2460 ATTGCTTGACATTTGAACACAGAGAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCA 2519
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length cDNAs defined in the specification, and for the detection and/or disgnosis of the abnormality of the proteins encoded by the full-length CDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                               Claim 3; SEQ ID NO 8501; 2537pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 515; DB 4; I Pred. No. 1.8e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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96.5%;
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Best Local Similarity 96.5
Matches 524; Conservative
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Human, colon cancer; colon tumour antigen; cytostatic; vaccine; colon tumour metastatic antigen; diagnosis; gene; ss.

Human colon tumour antigen polynucleotide SEQ ID NO:2040.

(first entry)

08-APR-2002

ABL38451;

BP.

ABL38451 standard; cDNA; 561

ABL3845

RESULT

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Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient.

Secrist

Jiang Y, Harlocker SL, WPI; 2002-114514/15.

(CORI-) CORIXA CORP

08-JUN-2001; 2001WO-US018557.

WO200196388-A2

20-DEC-2001

Homo sapiens

09-JUN-2000; 2000US-0210899P. 20-FEB-2001; 2001US-0270216P.

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TIGICALTITIGCACTITICAAAACTIAITITICITIGGAAAACAATAITIAIAGGGCTIAAAG 2902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAGCCCTGATAATGAAGGATGAACTAGTGATTTCTAATCCTCCCTTTTTTGATTT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGGATGTGCTTTTAAATGTCCTTTTGCCTGCATGAGGTGGAAAGGGGACCTTTTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 561 BP; 144 A; 91 C; 93 G; 226 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATTITICATITICIAATCIAAATTAIGIGIGICCIAICIG 2942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 9.0%; Score 265.8; DB 6; Best Local Similarity 96.4%; Pred. No. 5.1e-68; Matches 270; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 2040; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTACTCATACCTAGAAGGTGACCTTCCCATTTCTGCCAGACCAGCTTGTAGTAACAAA 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1499 ATAGAATTATTAACTACAGAGGTTCCACTTGCTTTTGGAAGAAGAGGGCCCTTCTGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCCATCTAGTGAGATACCTATGGAAAAGGAGCCTGGAGAGGGCCCGAATAAGTGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TGTCCATCTAGTGAGATACCTATGGAAAAGGAGCCTGGAGAGGGCCCGAATAAGTGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 33878; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 218 BP; 63 A; 42 C; 54 G; 59 T; 0 U; 0 Other;
243 CCCATTTTCATTTCTAATCTAAATTATGTGTGCCTATCTG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGATAGATTATATTTGGGAGGTGCATCCAGTGACCT 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 218; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 5.2e-54;
Matches 218; Conservative 0; Mismatches 0;
                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 33878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression and secretion vectors
                                                                                           AAC29803 standard; cDNA; 218
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                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dumas Milne Edwards J,
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                                                                                                                                                                      06-OCT-2000
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                                                                                                                                AAC29803;
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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK4450-ABK4621. Tepresent coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New colon cancer polypeptides and polymucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2774 TITIGATITAGITGGATGTGCTTTTAAATGTCCTTTGCCTGCATGAGGTGGAAAGGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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181 CTGATAGATTATATTTTGGGAGGTGCATCCAGTGACCT 218
                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding colon tumour protein, SEQ ID No 45.
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0; Mismatches 10
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                                                                                                                                                                                     BP.
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28-MAR-2001; 2001US-0279763P.
29-JUN-2001; 2001US-0302051P.
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                                                                                                                                                                                     ABK44494 standard; cDNA; 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-241739/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene; ss.
                                                                                                                                                                                                                                                          ABK44494;
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638

2833

2893

Length 399;

DB 8;

Query Match

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Claim 2; SEQ ID NO 2096; 38pp; English
                                                                                                                                Tao N,
                      ABX52167 standard; cDNA; 399 BP
                                                                                                 98US-0113678P.
                                                                                          26-OCT-2001; 2001US-00983965
                                     (first entry)
                                                                                                                                Mathialagan N,
                                                                                                            (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
                                                                                                                                       WPI; 2003-102386/09.
                                                                                                                        (WARR/) WARREN W C.
                                                                           US2002137160-A1
                                                                                                 17-DEC-1998;
15-DEC-1999;
                                      25-FEB-2003
                                                                                   26-SEP-2002.
                                                                   Bos Taurus.
                                                                                                                                Syatt JC,
                              ABX52167;
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The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second mucleic acid molecule comprising an electide sequences, appearing as ABX50072-ABX55983, or complements of them. Also included are cid in the call having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprishing: (a) incubating a marker nucleic acid (comprising any of the S912 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or transment) of the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for breading, preparation of comstnucts for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 5912 content of the molecule acid and the sequence was not shown in the specification but was obtained in the present content of the content of the molecule acid and the sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purified nucleic acid molecules, useful for genome mapping, gene identification and analysis, cattle breeding or preparation of constructs for cattle gene expression and genetically improved cattle.
                                                                                                          Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
Bovine EST associated with lactation/muscle/fat deposition #2096.
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2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTB are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                            161
                                                                                                                                                                                    221
                                                                                                                                                                                                                                              282 CTTCAAGCAAACATGTTTCAAAGGACTTAATGTTTTCGAGCAATGTTAAGATGATTCGA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                         2559 TGTAGTCCTAGCTAGCATACACTACCTCTTACCTGAGAGGTGTCTTTTAAAAACAAA 2615
                                                                                                                                                                                                                                                                                                                                                                                                            342 AGCCTCTGGCCCTAGCATACACTACCTCTTACTTGAGAGGGTACTTTTAAAAACCAA 398
                                                                                                                                                                     162 AGGACCATGGGAAGAATTTGCACGGGATGGATGCAGGTTCCAGAAACGAATTCAAGAAC
                                                                                                          102 ATAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTACATAAGCGGTGATGAGGATCGAAA
                                                                         2323 AAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATATAAGTGGTGATGAGGATCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 11013.
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Score 198.6; DB 8
Pred. No. 4.8e-48;
0; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC06938 standard; cDNA; 195 BP
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6.8%;
llarity 83.8%;
Conservative (
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                   Local Similarity
Les 249; Conserv
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Matches
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                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
                                                                                                                                                                                    CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGAGGCCGTGGGGGGACT
                                                                                                                                                                                                                                                                  CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGAGGCCGTGGGGGGACT
                                                                                                                                                                                                                                                                                                                                                   1 ATTITIGGCTTCGCTTCCACCGCACCAGCCGCCTACCCAGTCCTTCCGGTATCGCGTTG
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                                                                                Length 195;
                                                                                                                      0; Indels
                                        Sequence 195 BP; 33 A; 65 C; 54 G; 43 T; 0 U; 0 Other;
                                                                              Guery Match 6.6%; Score 195; DB 3; L
Best Local Similarity 100.0%; Pred. No. 3.6e-47;
Matches 195; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung small cell carcinoma antigen,
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  expression and secretion vectors
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01-SEP-2000; 2000US-0229763P.
05-SEP-2000; 2000US-0230629P.
14-SEP-2000; 2000US-0232565P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS61819 standard; cDNA; 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0196780P.
                                                                                                                                                                                                                                                                                                                                                                                                            AGTCGCATCAGTCGC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCGCATCAGTCGC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-010896/01
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200177168-A2
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AAS61819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTGAGGTGGAAAGGGGACCTTTTTGAGTTGTCATTTTGCACTTTCAAAACTTATTTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AASG1460-AASG1874 represent novel human lung small cell cancer antigen coding sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated polynucleotide (a) comprising any the 666 fully defined nucleotide sequences appearing as ADD49258 - ADD499315, ADD499316 and ADD499318, complements of (a); sequences of at least 20 contiguous residues of (a); sequences that hybridise to (a) under highly stringent conditions; sequences having at least 75 or 90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; lung cancer antigen; cytostatic; lung cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2754 GTGATTTCTAATCCTCCCTTTTTTGATTTAGTTGGATGTGCTTTTAAATGTCCTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2814 GCATGAGGTGGAAAGGGGACCTTTTTGAGTTGTCATTTTGCACTTTCAAAACTTATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGATTTCTAAATCCTCCCTTTTTTGATTTAGTTGGATGTGCTTTTAAATGTCCTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   Length 628;
                                                                                                                                                                                                                                                                                                                           Sequence 628 BP; 161 A; 101 C; 103 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                Score 187.4; DB 6;
Pred. No. 1.4e-44;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                             6.4%;
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ADD49398 standard; cDNA; 173
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                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 99.5
Matches 188; Conservative
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WO2003000898-A1

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identity to (a); or degenerate variants of (a). Also included are an isolated polypeptide (b) (comprising the acquences encoded by the new polypeptide, any of the 4 amino acid sequences fully defined in the specification; or sequences having at least 70 or 90% identity to the sequence in (a) or (b)), an expression vector comprising the above polyperide operably linked to an expression control sequence, a host call transformed or transfected with the above expression vector, an isolated antibody, or its antigen-blinding fragment, that specifically binds to the above polypeptide, an oligonucleotide that hybridises to the showe mentioned nucleotide sequences under highly stringen conditions, a fusion protein comprising a least one polypeptide cited above, detecting the parient; contacting the biological sample with a binding agent that binds to the polypeptide, or with the oligonucleotide cited above detecting in the sample an amount of polypeptide cited above, detecting an according of a cancer in a patient of the polypeptide cited above, detecting an expression of the polypeptide cited above, detecting agent, or an amount of a polymucleotide that hybridises to the binding agent, or an amount of a polymucleotide that hybridises to be binding agent, or atmilating and/or expanding and/or expanding and comparing and comparing of the polymucleotide, under conditions and for a time sufficient to permit the polymucleotide, under conditions and for a time sufficient to permit the component selected from physiological carriers and itse component selected from physiological carriers and surface polymetide, polymucleotide, under conditions and for a time sufficient to permit the above composition of a compariant comparising accompanies are proved to comparising a second component selected from the above composition and/or expansion of T-cells), an isolated T-cell population and intensity and antipon-presenting cells that express the above polypeptide, polymucleotide, an antibody fusion process in a patient (comprising a co
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CTGTCCTTTGACATTTTTTTTTTTAGAGGAAATGTAACTTGGATCTAGTTTAATTTTTTT 1; Gaps TGAACTAGTGTGATTTCTAATCCTCCTTTTTTTGATTTAGTTGGATGTGCTTTT 2798 Length 173; 0; Indels Sequence 173 BP; 73 A; 30 C; 28 G; 42 T; 0 U; 0 Other; Score 162; DB 10; Pred. No. 2.4e-37; 0; Mismatches 0; 5.5%; Best Local Similarity 99.4 Matches 173; Conservative 173 2625 2685 2745 Query Match 요 δ 셤 ઠે ò

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Plant; bacterial infection; fungal infection; viral infection; rice; ADA71938 standard; DNA; 2000 (first entry) Rice gene, SEQ ID 5263 20-NOV-2003 ADA71938; dB. gene;

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Oryza sativa

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is aignificantly altered in the interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to 1705 ATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGATTGGGATGAGGAAGCTGA 1764 1765 GGATGATGGTTTTGATAGTGATAGCTCACTGTCAGACTCAGACCTTGAACAAGACCCTGA 1824 1825 AGGGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTAC 1884 1885 AGCAACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCTTCTGATTCAGAGAAGGA 1944 TITGICIGGCAAGICIGAICIAGAGAATICCICCCAGICIGGAAGCCTICCIGAGACCCC 2004 3125 TCCTTTTCAAACATCAGGGGAAAATGAGAAAGGCTGTCGTGACTCAAAGACCCCATCTGA 2184 1185 GTCCATTGTGGCCATTTCTGAGTGTCACACCTTACTTTCTTGTAAGGTGCAGCTGTTGGG 2244 278 YSWSYKWWMCTAYKK---SYYSRWCYMYRGGGWRGATRYWGRGYMSRWAMMYKKWYRG 334 394 KRKYKRMRGYSRMRSCKRARMMKRCRSGRAWKMGCRGCRGCMTCRMKSYGMRWKSWKRMASK 453 335 YKGMKRGWAGRAMMRSMCRWS-KACYYMRWRWWRMTRRRRWAKKSRTSRRKKRKWCMR 393 454 YKWASRMYRWEKKKCSRTTMWGKTRGGMMGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRW 513 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant 218 SRKYGTYKKMTYYSASRCMRAYMTTSYSWACSSYTWCRSKRRSWMWKMMRKMRKSKYGW ::: | :: | :: | :: | :: | | :: | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 | | 1.1 TGAGCATAGTTCTGGGGAGGAAGATGACTGGGAATCTAGTGCAGATGAAGCAGAGAGTCT 1065 CAAACTGTGGAACTCATTCTGTAATTCTGATGACCCCTACAACCCTTTAAATTTTAAGGC 574 KYSKCSWYCKMSYYASCMKSARKAGAKMCKRSKMSKMSKSMRSSRKCRKCASKRSSAKRY ö Hou Y; 2.1%; Score 61.8; DB 8; Length 2000; Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other; SA, Hou Zhu T, Indele Glazebrook J, Goff Whitham S, Xie Z, Matches 110; Conservative 402; Mismatches 414; Pred. No. 1e-06; Claim 27; SEQ ID NO 5263; 899pp; English (SYGN) SYNGENTA PARTICIPATIONS AG. Cooper B, 22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105 illustrate the invention. Chang H, Chen W, Cc Katagiri F, Quan S, WPI; 2003-175290/17. Local Similarity gene expression 03-JAN-2003 1945 2005 셤 ઠ ద 8 원 8 셤 ò 셤 ઠે 셤 ઠે 셤 ठ à 셤 ð

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2305 CACACATGTCAAAAGAAAAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATATAAG 2364
                                                                                                                    2485 AAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTCTCAAGCAATG 2544
                                                                                                                                                                                                                                                                  2545 ITGAGTIGGCAGCCIGIAGICCIAGCIAGCAIACACIACCICTIACCIGAGAGGIGICII 2604
                                                                                                                                                                    GAAACGAATTCAAGAAACAGAAGATGCTATTGGATATTGCTTGACATTTGAACACAGAGA 2484
                                                                                                                                                                                  634 AMMGGMTSGSRMSRWKSYTC-----YWRKWGSMKSTCTWMYYMSKYTYAKYGSYWRYR 686
                                                                                    147 WYYWSWWWARTWRWWRRYATRMWWWYRYSWRYWTWCTWWGYWWTTWRTYMKMRYWWYKC 806
                                                                                                                                     |: :: || || : :: 807 IKTYWYWSATYWTGTWAAWWMXKTKWRMGMTGAKTRGRAARKARYWWKWATWCATKRWMTK 866
                                                                                                                                                                                                                                  927 KOMWINIKGGRINGWIKYWYWYCTIWKAACGRAIKYMCCAGWWAMYSYSWIRIYWMRIWRHW 986
                                                                                                                                                                                                                                                                                                                                   TTAAAAACAAATCTTGGCAGCTGTCCTTTGACATTTT 2641
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Search completed: September 15, 2005, 16:13:36 Job time : 1436.17 secs

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50 S S S S S S S S S S S S S S S S S S S	US-09-471-275-750 US-09-471-276-750 US-09-949-016-4642 US-09-949-016-4642 US-09-949-016-1554 US-09-949-016-1554 US-09-949-016-1137 US-09-949-016-1471 US-09-328-352-1597 US-09-328-352-1597 US-09-328-352-1597 US-09-328-352-1597 US-09-349-016-1471 US-09-270-767-3435 US-09-614-221A-345 US-09-614-221A-345 US-09-949-016-1670 US-09-949-016-1670	US-09-248-79-018-13 US-09-248-796A-7 US-09-949-016-17 US-08-906-155A-4 US-09-746-801A-3 US-09-134-000C-3 US-09-134-000C-3 US-08-906-155A-2 US-08-906-155A-2 US-09-902-540-58 US-09-902-540-58 US-09-902-540-16 US-09-902-540-16 US-09-902-540-16 US-09-902-540-16 US-09-902-540-16 US-09-902-540-16 US-09-902-540-16	US-09-577-902-1 US-09-140-749-64 US-07-991-8678-41 US-08-306-1267-41 US-08-306-1267-11 US-08-140-749-1 US-08-140-749-1 US-09-140-749-1 US-09-140-749-1 US-09-349-016-15420 US-09-349-016-15420 US-09-349-016-15420 US-09-349-016-1432 US-09-349-016-14970 US-09-349-016-14970 US-09-349-016-14970 US-09-349-016-14970 US-09-349-016-14970 US-09-349-016-204315 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-349-016-74412 US-09-348-796A-4637 US-09-348-796A-4637 US-09-347-8554-5 US-09-497-8554-5
8 1.3 8677 8 1.3 34261 8 1.3 49309 8 1.3 49309 8 1.3 85368 9 1.3 462589 8 1.3 462589 6 1.3 46044	1.3 410 1.3 410 1.3 696 1.3 696 1.3 74881 37 1.3 74881 37 1.3 74881 37 1.3 74881 37 1.3 74881 1.3 2299 1.2 2295 1.2 2295 1.3 46288		36 1.2 1212 3 36 1.2 1212 3 36 1.2 1689 1 36 1.2 1689 2 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 1689 3 36 1.2 8457 1 36 1.2 8457 2 4857 8 5.8 1.2 8457 8 5.8 1.2 8457 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.8 1.2 12772 8 5.9 1
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: September 15, 2005, 12:27:30; Search time 439.026 Seconds (without alignment on the search time 439.026 Seconds to the search time 439.026 Seconds the search time 439.0	refrecacaaattatgtgtgcctatctg 2942 pext 1.0 18138359 residues 1 chosen parameters: 2405568	Database: Issued Patents Na: Issued: Issue	No. Score Match Length DB ID 2

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Sequence 33878, Application US/09513999C

Patent No. 6783961

GENERAL INPORMATION:
APPLICANT: Dunas Mille Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT APPLICANT: US/09/513,999C

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 33878

LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TITIGGGCTICGCTICCACCGCACCAGCCGGCCTACCCAGICCTICCGGTATCGCGTIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OP INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.4%; Score 219; DB 4; 96.4%; Pred. No. 2.3e-56; Live 4; Mismatches 4.
ALIGNMENTS
                                                               US-09-621-976-8778
Sequence 8778, Application US/09621976
; Patent No. 6639063
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 68,76..78
OTHER INFORMATION: n=a, g, c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.4 Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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US-09-513-999C-33878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11013, Application US/09513999C
; Sequence 11013, Application US/09513999C
; Sequence 11013, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Duclett, A.
; APPLICANT: Duclett, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PILE REPERBING: 59.US2.REG
; FILE REPERBING: 159.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER: OF SEQ ID NOS: 36681
; SEQ ID NO 11013
; LENGTH: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAGGGGCTTTTCAACCCTCTGTCAGTCGGAAAACCATCGCCGAGGCCGTGGGGGGGACT 120
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                                                                                                                                         1559 TGTCCATCTAGTGAGATACCTATGGAAAAGGAGCCTGGAGAGGGCCGAATAAGTGTAGTT
                                                                                                             1 ATTITIGGCTTCCCTTCCACCGCCCACCAGCCGCCTACCCCAGTCCTTCCGCGTATCGCGTTG
                                                          Gaps
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Length 218;
                                                     Indels
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Best Local Similarity 100.0%; Pred. No. 4.5e-49;
Matches 195; Conservative 0; Mismatches 0;
  7.4%; Score 218; DB 4; 100.0%; Pred. No. 4.5e-56; Live 0; Mismatches 0;
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; Sequence 14, Application US/08232463
; Patent No. 5570367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AGTCGCATCAGTCGC 195
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  Query Match
Best Local Similarity 100.0
Matches 218; Conservative
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ORGANISM: Homo sapiens
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TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                             NAME/KEY: promoter
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                                                                                                                                                                  SEQ ID NO 22
LENGTH: 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2348 ACTGAGTATTATATAAGTGGTGATGAGGATCGCAAAGGACCATGGGAAGAATTTGCAAGG 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2408 GATGGATGCAGGTTCCAGAAACGAATTCAAGAAACAGAAGATGCTATTGGATATTGCTTG 2467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 1.7%; Score 51; DB 1; Length 7218; Il Similarity 3.7%; Pred. No. 0.00076; 12; Conservative 189; Mismatches 124; Indels
                                                                                                             ZIP: 22313-0229
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
                                                          Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1070 RRRRATCGCAAGCTCCCTCGACCTG 1046
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                                                                                                                                                                                                                                                        CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
              NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Landner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F18 US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                       Alexandria
                                                                                                       USA
                                                                                                                                                                                                                                           FILING DATE:
                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX:
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US-09-806-708B-22/c ; Sequence 22, Application US/09806708B

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LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1833 ACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAGCAACAA 1892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1773 GTTTTGATAGTGATAGCTCACTGTCAGACTCAGACCTTGAACAAGACCCTGAAGGGCTTC 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    893 ITCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCTTCTGATTCAGAGAAGGATTTGTCTG 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1953 GCAAGTCTGATCTAGAGAATTCCTCCCAGTCTGGAAGCCTTCCTGAGACCCCTGAGCATA 2012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1433 TTCAAGAAACAGAAGATGCTATTGGATATTGCTTGACATTTGAACACAGAGAAGAATGT 2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               914 TACYNRAATHNKWATHWKWTHGAHSKRRTRHHTRTCRRTKYNNNNNARTVYWYHHAAR 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              854 RW------MNAWWIRINNNNNNNNNACRNIRIWWABWKHSWCNNNNNNNNNNNNNWWW 802
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GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT PAPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 45.4; DB 4; Length 1141; 11.6%; Pred. No. 0.01;
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Matches 109; Conservative 325; Mismatches 498;
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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Fatent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11893
LENGTH: 45365
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Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                             8613 AAATCTTGGCAGCTGTCCTTTGACATTTTTTTTTTAGAGGAAATGTAACTTGGATCTAG 2672
                     263 RYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRRABHRSWNMWWVKCRNKYMVSW 204
                                                                      2553 GCAGCCTGTAGTCCTAGCTAGCATACACTACCTCTTACCTGAGAGGTGTCTTTTAAAAAC
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Pred. No. 1.1;
0; Mismatches 109; Indels 0;
                                                                                                                                                                                                                    2673 TITAATITITITITIGCAACATATCCCACTCAGAAACATT 2713
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Best Local Similarity 49.8%;
Matches 108; Conservative C
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US-09-949-016-11893
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ORGANISM: Human
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19684 AAAGTAATTAATTAAATTCCAGGCCTTTTAATGAACAGTCTTCTGCTTTTTTCTCTTTAACA 19743
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Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFRENCE: GENSET.054PR.
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17202
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 17007
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Pred. No. 1.
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RESULT 11
US-09-949-016-15525
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189 WMKKGSRRRATSRYGMMSSMYGASKRMSSMCSASTRMSSASCMYYMMSAGSYASCAWKM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 TSRGSYRRYKTSAMMGRAKOKKKKKKKKKKKKKGGGKKGGGTYMAMRSRRGSTGRWSYRR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 AMWRGSKSWGWGGSYYRMAGYRSSRWRSWYSAMWRKKKMTCWKGRSSWGSRSTGYYAWMYK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 KSWCTSRKWMYYKKRRKKKRRKCTST-----KRTCYRGSTYKCWKAYYTKKRRKWTRW 159
                                            CGGGTCAGTTACTGGACGAAACTGCTCTCCCAGCTCCTTGCGCCGCTCCCCGGATTGCTT 640
                                                              SKYRRCAKWSCTYSWYMRASMKKSKYCAWSRKGSKCCMYSRKGSKSCYCCWGGSCCCCGC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT PAPLICATION NUMBER: US/09/806,708B
CURRENT PILING DATE: 2001-04-03
PRIOR PILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
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1.4%; Score 41.4; DB 4; Length 399;
Best Local Similarity 19.5%; Pred. No. 0.077;
Matches 56; Conservative 114; Mismatches 110; Indels
                                                                                                                                                                                                        Sequence 8976, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8996
LENGTH: 399
                                                                                                       CAGAAGGTGCTAATTTGGAGCC 662
                                                                                                                                  cadcadecaderacerdece 330
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                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8976
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Sequence 15525, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                          B.n. FAE1 promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2651 AGGAAATGTAACTTGGATCTAGTTTAATTTTTTTTTTGCAACATATCCCACTCAGAAAC 2710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2475 AACACAGAGAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTC 2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2711 ATTCAGGTTTGAAGCCAGCCCTGATAATGAAGGATGAACTAGTGTGTGATTTCTAATCCTCC 2770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 MCKRKVRRWVRTRGRMRNYWVAWBTAHRRRYNNGWTBAMAYRRWTMNNNNNAKAMCKRA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 NNWTYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTWVNNNGTTMWKRWWA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 WYWKMDMDWBGTYNNNNNGGRTYYGWTKNKKOWTYYKWKANNCKWRAWDHKTCTHNNTTW 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 CSKWWNNYAAMYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHYGYKWNTR 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653 NNATCARDDYYAASRWYAMANAKWYYYKBAANNAYYTHANNWWGCWNWATDTRRTMWKNN 712
                                                                                                                                                                                                                                                                                                                                                                           173 TGWDDDTKYHMWINNGCBTVTWMVRYKTDRDWSBKRMNYGMBWKNWSYDVTYYWWVMDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 KYMGWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : : : : : | | :: | :: | | :: | 413 WKMKIYWINNWDYWKACIWYKYBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2175 CCCCATCTGAGTCCATTGTGGCCATTTCTGAGTGTCACACCTTACTTTCTTGTAAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4,
                                                                                                                                                                                                                       Length 1141;
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                                                                                                          ; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and US-09-806-708B-22
                                                                                                                                                                                                                       Query Match
1.4%; Score 40.8; DB 4;
Best Local Similarity 9.0%; Pred. No. 0.26;
Matches 65; Conservative 291; Mismatches 363;
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
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Sequence 1177, Application US/09023655
; Sequence 1177, Application US/09023655
; Retent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; APPLICANT: Susan G. Stuart
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; COUNTERSPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PRARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1688 TATATTTTGGGAGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGAT 1747
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1064 GCGGATGAGGAAGGAAGAAGAAGAGAGATGAGGAAAATGATCCAGACTATGACCCAAAG 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CIASSIPTCATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1808 CTTGAACAAGACCCTGAAGGG 1828
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                                                 1808 CTTGAACAAGACCCTGAAGGG 1828
                                                                                             1124 AAGGATCAAAACCCAGCAGAG 1144
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1177:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Tea 78; Conserve
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US-09-023-655-1177
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

FRIOR PILING DATE: 2000-10-20

FRIOR PILING DATE: 2000-10-03

FRIOR PILING DATE: 2000-10-03

FRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 3573

LENGTH: 1468
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 117807;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 40.4; DB 4;
51.1%; Pred. No. 11;
tive 0; Mismatches 91;
                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
SPRIOR PLING DATE: 2000-10-03
SOFTWARE: PASELSE OF WINDOWS VERSION 4.0
SSOFTWARE: PASELSEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: PASELSEQ FOR WINDOWS VERSION 4.0
SERVITH: 117807
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.1
Matches 95; Conservative
    FILE REFERENCE: CL001307
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Matches 78; Conserv
                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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                                                                      APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GRNES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-00135 U3 CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PLING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 334
LENGTH: 4252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1688 TATATTTTGGGAGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGAT 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1300 GCGGATGAGGAAAGGGGAAGAAGAAGAGGAGATGAGGAAAATGATCCAGACTATGACCCAAAG 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.2; DB 4; Length 4252;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1;
0; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    , LOCATION: 1730, 1747, 1751, 1763, 1769, 1771-1772, 1778
, OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INPORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6727066 995575.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1808 CTTGAACAAGACCCTGAAGGG 1828
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                Sequence 334, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
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US-09-919-039-334
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US-08-232-463-14
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Best Local Similarity 6.4%; Pred. No. 2.3;
Best Local Similarity 6.4%; Pred. No. 2.3;
Matches 27; Conservative 208; Mismatches 187; Indels
                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)693-4109
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EP 91 114 300.6
                                                                                                                                                                         TELEFAX: (703)683-4109
TELEX: 899149
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                  FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER:
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US-08-232-463-14
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Scoring table:

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Sequence 2040, Ap Sequence 2040, Ap Sequence 45, App1 Sequence 45, App1 Sequence 45, App1 Sequence 2096, App Sequence 12337, App Sequence 2179, App Sequence 134, App Sequence 1179, App Sequence 1174, App
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10 US-10-35-99-5801

17 US-10-424-599-5801

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10 US-09-814-353-17220

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10 US-09-814-353-17220

10 US-09-80-107-2410

15 US-10-146-473-30

16 US-10-641-643-1177

22 US-10-450-763-16737

16 US-10-269-999-53

16 US-10-269-999-54

16 US-10-269-999-55
3 US-10-046-935-2040
4 US-10-146-502-2040
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1411	1921 AGAGCCTTCTGATTCAGAGAGATTCTGTCGCAGTCTGATTTGAGAATTCCTCCCC 1980

Qy 1776 TTGATAGTGATAGCTCACTGTCAGACTTGAGACCTTGAAGAGCCTTGAAGAGGCTTCACC	QY 1836 TTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAACTTTACAGCAACAATTC	1896	1956 1532	2016 1592	2076	OY 2136 CATCAGGGAAAATGAGAAAGGTGTCGTGACTCAAAGACCCCATCTGAGTCCATTGTGG	Qy 2196 CCATTCTGAGTGTCACCCTTACTTTCTAAGGTGCAGCTGTTGGGGAGCCAAGAAA	Qy 2256 GTGAATGTCCAGACTCGGTACAGCGTGACGTTCTTTCTGGAGGAAGACACACAC	2376	2436	2496	Oy 2556 GCTGTAGTTGCTAGCATACACTACCTCTTACCTGAGAGGTGTCTTTTAAAACAAA	Qy 2676 AATTITTTTTTGCAACATATCCCACTCAGAACATT-CAGGTTTGAAGCCAGCCCT-G	Oy 2734 ATRATGARGATGAACT 2750 	RESULT 3 US-09-925-299-168 ; Sequence 168, Application US/09925299
212 TGCTTCAGAAGGTGCTAATTTGGAGCCAACTTTTCGGTGGAATGTTTCCGACCAGATGGC 271 696 TAGATTTTGCTGGAGTCTACAGCGCCCTGAAGAGCCCTGAAGGGACGGAGAAACCAGCG 755		CCAGTCCCCTTGATTGGCTAGAGAGGGATCCACTGGCAATACTCGCCCCAGACCTAA	876 AATTGGAGCTTAAGGCCAAGGGAAGTGCTTTGGACCCTGCAGGCAG	936 AGCAGCAGCTGTGGGGGGTGTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTA 995	996 ACCGGGAACTTGGCTCTTCGCCCTCTGAACATTCAACGCATGGACATTTCA 1055	1056 GTGTGGTATCCTATTTGCTGAACCCTTCCTACGCTGCTTTCCTAGGCTAGAAGTCA 1115	GCTATCAGAACAGTGATGGAAATAGCGAGGTAGTTCGGCTTCCAGACACTAACCCCAGAGA			1356 ACCAGGATAATGGCTACCACAGCCTGGAGGAGGAGCACACACGCTTCTCCGGATGGAT	1416 AACACTGCAGAGATAACCCAACACAGTTTGTTCCTGCTGGAGACATTCCTGGAACA 1475 	1476 CCCAGGAATCCACTGAAGAAAAATAGAATTATTAACTACAGAGGTTCCACTTGCTTTGG 1535 		CCAGACCAGCTTGTAGTAACAACTGATAGATTATATTTTGGGAGGTGCATCCAGTGACC 	1716 IGGAAACAAGIICIGAICCAGAAGGIGAGGAITGGGAIGAGGAAGCIGAGGAIGAIGGIT 1775

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                                    SCTCGTGGCAGGGATGTCCACCTCTTTCTACGGAAGGCCTACCAGAAATTCACCATCTTC
                                                                                       CCCAGGAATCCACTGAAGAAAAAAAAATAGAATTATTAACTACAGAGGTTCCACTTGCTTTGG
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                                       and Antibodies
       GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: FALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: FOT/US00/05883
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEC ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 168
                                                                                                                                                                                                                                          Score 2185.8;
Pred. No. 0;
6; Mismatches
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.9%;
Matches 2249; Conservative
 US20030040617A9
                                                                                                                                                                                                    ) ORGANISM: Homo sapiens
US-09-925-299-168
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Oy 2316 AAAGAAAAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATATAAAGTGGTGATGAGG 2375	2376 ATCGCAAAGGACCATGGGAAGAATTTGCAAGGGATGGATG	DD 1952 AICGCAAAGGACCAIGGGAAGAATITGCAAGGGAIGGAIGCAGGAACGAATIC ZULL Qy 2436 AAGAAACAGAAGATGCTATTGGATTTGACATTTGAACACAGAAGAATGTTA 2495	Db 2012 AAGAAACAGAAGATGTTTTTTTTTTTTTTTTTTTTTTTT	2072 ATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTCTCAAGCAATGTTGAGTTGGCA	OY 2556 GCCTGTAGTTGGATAGCTTACCTTACCTGAGAGGTGTCTTTTAAAAACAAA 2615	Qy 2616 TCTTGGCAGCTGTCCTTTGACATTTTTTTTTAGAGGAAATGTAACTTGGATCTAGTTT 2675 Db 2192 TCTTGGCAGCTGTCCTTTGACATTTTTTTTTTTTTTTTT	2676 AAITTITITITIGCAACATATCCCACTCAGAACATT-CAGGTTTGAAGCCAGGCCT-G	2734 ATAATGAAGATGAACT 2750 		RESULT 4 02-10-60-482-3 ; Sequence 3, Application US/10650482 ; Publication No. US20040142345A1	; GENERAL INFORMATION: ; APPLICANT: Ron, David ; APPLICANT: Jousse, Celine ; TITLE OF INVENTION: METHODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN elF2alpha-6	; TITLE OF INVENTION: PHOSPHATASE SUBUNIT; PILE REFERENCE: 598(AL1/12-US); CURRENT APPLICATION NUMBER: US/10/650,482; CURRENT FILING DATE: 2003-08-28	; PRIOR APPLICATION NUMBER: US 60/408,679 ; PRIOR FILING DATE: 2002-09-06 ; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: Patentin version 3.1	; SEQ ID NO 3 ; LENTH: 5468 ; TYPE: DNA ; ORGANISM: Mus musculus	US-10-650-482-3 Query Match Best Local Similarity 72.5%; Pred. No. 0;	Matches 1964; Conservat 96 CCATCGCCGAGG	156 GAACCTCCC-CGCCAGGATGGATGGATGCATCAGTCGCCCCCTTTCCGCGCGCCTGT	211 ACGTCTCCTTCCCTAGGCCGGGATGGACCTAACCGCGGGTCGCCACGCCTTGCGCGGGGCCTC 215 TCTTCCCTGTGCTGCCGCCGCTGCCGATTCGCTGCCCTCTGTGGCTTTTCTGCTGG	DD 271 TGGGCGGTCCGGTGCAGCACTCGTTGCGGAAAGCCGCCGCTCTCTGGGCCTGCCGGG 330 Qy 275 CTCGAAGATCGGCCTGGAGCAGCGACGCCACCGCTGGGCCAAGGCCGAGACTCTGTAGGCT 334

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Sequence 2040, Application US/09878178

GREREAL INCORMATION:

APPLICANT: Harlocker, Susan L.

APPLICANT: Gentiet, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

TITLE OF INVENTION UNMBER: US/09/878,178

CURRENT RELING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 2237

SEQ ID NO 2040

LENGTH: 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or
US-09-878-178-2040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
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US-09-878-178-2040
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Sequence 3997, Application US/10756149

GENERAL INFORMATION:

APPLICANT: Albert:

TITLE OF INVENTION: METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER FILE REFERENCE: file

CURRENT APPLICATION UNDER: US/10/756,149

CURRENT APPLICATION UNDER: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

SOFTWARKE: PATENTING DATE: 2004-01-12

SOFTWARKE: PATENTING DATE: 2004-01-12

SOFTWARKE: PATENTING APPLICATION UNDER: 2018

SEQ ID NO 3997

LENGTH: 465
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                                          ---CTGTGGAACTCATTCTGTAA---TTCTGATGACCCCTACAACCTTTAAATTTTAAG
                                                                                361 ACTGTGGGAACTTCATTCTGTTAATTCTGGATGGACCCCTACAAACCTTTAAATTTTTAAG
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Pred. No. 1.9e-119;
0; Mismatches 2;
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Best Local Similarity 99.1%;
Matches 459; Conservative
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CORGANISM: Homo Sapiens
US-10-756-149-3997
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Bublication No. US20030069180A1

GENERAL INFORMATION:

APPLICANT: Jiang, Yuqiu

APPLICANT: Harlocker, Susan L.

APPLICANT: Stolk, Heather

APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS AND INTITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

TITLE OF INVENTION: COMPOSITION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITION: STOLE OF COLON CANCER

TITLE REFERENCE: 210121.527C2

CURRENT PAPLICATION NUMBER: 2002-05-14

NUMBER OF SEQ ID NOS: 2241

NUMBER OF SEQ ID NOS: 2241

SEQ ID NO 2040

LENGTH: 558
                                                JERUBICANT: Jiang, Yuqiu

APPLICANT: Jiang, Yuqiu

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Heather

APPLICANT: Harlocker, Heather

APPLICANT: Wang, Aijun

APPLICANT: Wang, Aijun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER

TITLE OF INVENTION: WAND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.527C1

CURRENT APPLICATION NUMBER: US/10/046,935

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 2239

SOFTWARE: FOREISE FOR Windows Version 4.0

LENGTH: 558
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Best Local Similarity 96.4%; Pred. No. 2.5e-68;
Matches 270; Conservative 0; Mismatches 10
               Sequence 2040, Application US/10046935
Publication No. US20020156011A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 8, 9, 14, 354, 527
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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// OTHER INFORMAT:
US-10-046-935-2040
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                                                                                                                                                                 DB 14; Length 558;
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                                                                                                                                                                                       .5e-68;
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96.4%; Pred. No. 2.5e
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; Sequence 45, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: 8, 9, 14, 354, 527
; CTHER INFORMATION: n = A,T,C or
US-10-146-502-2040
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| LOCATION: 34, 35, 39
| OTHER INFORMATION: n = A,T,C or
US-09-920-300A-45
                                                                                                                                                                                       Best Local Similarity 96.4
Matches 270; Conservative
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US-10-961-527-45/c
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2894 GGCTTAAAGCCCCATTTTCATTTCTAATCTAAATTATGTGTGCCTATCTG 2942
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                                                                                                                 US-10-033-528-45/c

| Sequence 45, Application US/10033528
| Publication No. US20020131971A1
| GENERAL INFORMATION:
| APPLICANT: Nu. Jiangchun
| APPLICANT: Meagher, Madeleine Joy
| APPLICANT: Secrist, Heather
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| TURNERT APPLICATION UNDRER: US/10/033,528
| CURRENT FILING DATE: 2001-12-26
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 45
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| Sequence 45, Application US/1009926
| Publication No. US20030166064A1
| GENERAL INFORMATION:
| APPLICANT: King Gordon E.
| APPLICANT: Xu, Jiangchun
| APPLICANT: Secriet, Heather
| APPLICANT: Secriet, Heather
| APPLICANT: Secriet, Heather
| TITLE OF INVENTION: AND DIAGNOSITS OF COLON CANCER
| TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
| PILE REFERENCE: 210121.547C2
| CURRENT APPLICATION NUMBER: US/10/099,926
| CURRENT FILING DATE: 2002-03-17
| NUMBER OF SEQ ID NOS: 1982
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 45
| LENGTH: 706
                       517 GGCTTAAAGCCCATTTTCATTTCTAAATTATGTGTGCCCTATCTG 469
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Best Local Similarity 94.8%; Pred. No. 3.4e-48;
Matches 217; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
i LOCATION: 34, 35, 39
CTHER INFORMATION: n = A,T,C or G
US-10-033-528-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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FUBLICATION NO. US20050147615A1

GENERAL INFORMATION:

APPLICANT: King, Gendle in Joy

APPLICANT: King, Jangchun

APPLICANT: Wing, Jangchun

APPLICANT: Wing, Jangchun

APPLICANT: Wing, Jangchun

TITLE OF INVENTION: OMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210.121.5474

CURRENT APPLICATION NUMBER: US/10/961,527

CURRENT FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: US 60/302,051

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PLING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 1789

SEQ ID NO 45

LENGTH: 706
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                                                                                                                                  Score 199; DB 16;
Pred. No. 3.4e-48;
0; Mismatches 10;
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6.8%; Score 199; DB 22;
Best Local Similarity 94.8%; Pred. No. 3.4e-48;
Matches 217; Conservative 0; Mismatches 10;
NAME/KEY: misc_feature

CCATION: 34, 35, 39

CTHER INFORMATION: n = A,T,C or G

US-10-099-226-45
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LOCATION: 34, 35, 39
OTHER INFORMATION: n = A,T,C or
                                                                                                                                        6.8%;
                                                                                                                                     Query Match
Best Local Similarity 94.8'
Matches 217; Conservative
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ORGANISM: Homo sapiens
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Search completed: September 16, 2005, 10:39:57 Job time : 1746.36 secs
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Patent No. US20020137160A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Mathialagan, Nagappan

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REPREDENCE: 37-21 (10297)

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: US 09/465,231

PRIOR APPLICATION NUMBER: US 60/113,678

PRIOR APPLICATION NUMBER: US 60/113,678

PRIOR APPLICATION NUMBER: US 60/113,678

NUMBER OF SEQ ID NOS: 5912

LENGTH: 399

LENGTH: 399
2834 CTTTTTGAGTTGTCATTTTGCACTTTCAAAACTTATTTTCTTGGAAAACAATATTTATAG 2893
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                                        102 ATAGGTAACCTTCCTTGAGAAGTTACTGAGTATTACATAAGCGGTGATGAGGATCGAAA 161
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Patent No. US20020068288A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Longtong
APPLICANT: Wang, Tongtong
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: 32-LIB3057-012-Q1-K1-H11
US-09-983-965-2096
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Matches 249; Conserve
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US-09-983-965-2096
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US-09-833-790-371
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                                                                                                                                                                                                                                                  Length 628;
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Pred. No. 9.5e-45;
0; Mismatches 1;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SEQ ID NO 3'11
LENGTH: 628
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Best Local Similarity 99.5%;
Matches 188; Conservative
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CORGANISM: Homo sapiens
US-09-833-790-371
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Oiagen (Hilden/Germany) within the CDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp66f1186) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzbi.de/cgi-bin/productscl.cgi?CloneID=DKFZp6661186
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                              HSM805059 3941 bp mRNA linear HTC 22-SEP-2004
Homo sapiens mRNA; cDNA DKFZp6661186 (from clone DKFZp6661186).
AL833746
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DLEGDPEGLHLWNSFCSVDPYNPQNFTATIQTAARIVPEBFSDSEKDLSGKSDLENS
OSGSLPETPERISGEBDDWESSADEAESLKLWNSFCNSDDPYNPLNFRAPFOFSGENS
KGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKK
VTPLEBVTEYYISGBBRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNR
LQGTCFKGLNVLKQC"
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BI088423 602852920
AI684846 wa86c12.x
                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1941)
Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="R2DD:DKF2p6661186"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="DKF2p6661186"
/tissue_type="stomach"
/clone_lib="666 (synonym: hsto2). Vector pSport1; host
DH10B; sites mot1 + Sal1"
/dev_stage="adult"
/note="hypothetical protein, N-terminus truncated"
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Pred. No. 0;
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GGAGGAACACACCCTTCTCCGGATGGATCCAAAACACTGCAGAGATAACCCCAACACAGTT
                         GGAGGAACACAGCCTTCTCCGGATGGATCCAAAACACTGCAGAGATAACCCAACAGTT
                                                                                    TGTTCCTGCTGCTGGAGACATTCCTGGAAACACCCCAGGAATCCACTGAAGAAAAATAGA
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Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530022L24 product:hypothetical protein, full insert sequence.
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                        CTCTTACCTGAGAGGTGTCTTTTAAAAACAAATCTTGGCAGCTGTCCTTTGACA-TTTTT 1319
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
CTTGACATTTGAACACAGAGAAAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAAGG
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The FAWING CORDSTELLED

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

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Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Ryashida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

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Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Saaaki, D., Sahibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

All Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of

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RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail:genome-resegge: riken:jp,

RESEAUSE CHARLED (16-APR-202)
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Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
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                            FANTOM CONSORTIUM.
FUNCtional annotation of a full-length mouse cDNA collection
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                                                                                                                      Nature 409, 685-690 (2001)
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GCGCGCGAAAACCCCAGACCCCCCCCAACCCCCAACCCCCAACCCCCAACCCCCC	2015 TCTGGGGAGGAAGTGGGAATTTGGTGCAGAGAGAGAGAGA
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Adachi, J., Azizawa, X., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiraoka, T., Harozane, T., Hori, F., Imotani, K., Ishii, Y., Kondo, S., Konno, H., Kasuka, T., Kauka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koda, M., Nakamira, M., Nishi, K., Nomura, K., Numazaki, A., Murata, M., Nakamira, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Okazahi, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission and Hayashizaki, Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegge:riken.jp, REX:81-45-503-9216)
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RGESLPVSTRPVCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSES
DVEQDSEGLHLWNSFHSVDPYNPQNFTATIQTAARIAPRDFSDSGTSWSGSCGVGSCO
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PSYLDYLPQLGLRCQSSAGGGPVGFRTLTPESCYLSEDGCHPQPLRAEMSATAWRRC
PPLSTEGLPEIHHLRMKRLEFLQANKGQELPTPDQDNGYHSLEEEHNLLRMDPQHCTD
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                                                                                                              The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2731)
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                            of a full-length mouse cDNA collection
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
FANTOM Consortium.
Functional annotation of a
Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2495 AATAGACTCCAGGGAACATGCTTCAAAGGACTTAATGTTCTCAAGCAATGTTGAGTTG-G 2553
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                                                                                                                                                                                                                   2275 AAGAGAAAAAGGTAACCTTCCTGGAAGATTACTGAGTATTATATAAGTGGTGATGAG 2334
                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTTCTCTGGCCATCATACCTTACTTGTAAGGCCCCAGCTGTTAGAGAGCCAAGAA 2214
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                      AAAAGAAAAAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATATAAGTGGTGATGAG
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High-efficiency full-length cDNA cloning
Meth. Brzymol. 303, 19-44 (1999)
9279253
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	1202 CATCCCCAGCCGCTGAGTGCAGAACTCATT		1123 TCTACAGAAGGCCTGCCGGAAATCCACAC		1382 GAGGAGGAACACAGCCTTCTCCGGATGGAT 	1442 TITGITCCTGCTGCTGGAGACATTCCTGGA 1300 GCGGTGTCCCCTGCTGCAGACAGGCC		1562 CCATCTAGTGAGATACCTATGGAAAAGGAG 	1622 TACTCATACCTAGAAGGTGACCTTCCCATT'	1682 ATAGATTATATTTTGGGAGGTGCATCCAGT			1862 CCTTATAATCCCCAGAACTTTACAGCAACA. 	1922 GAGCCTTCTGATTCAGAGAAGGATTTGTCTY	1982 TCTGGAAGCCTTCCTGAGCACTGAGCATI	2042 AGTGCAGATCAAGCAGAGAGTCTCAAACTG 	2102 TACAACCCTTTAAATTTTAAGGCTCCTTTTT 1930 TACAACCTTTTAAATTTTAAGGCTCCTTTTTTTTTTTTT		2222 TCTTGTAAGGTGCAGCTGTTGGGGGAGCCAA 2050 TCTTGTAAGGCCAGGTGTTAAAGAGCCAA
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Matches 1957; Conservative 0; Mismatches 641; Indels 79; Gaps 13;	TATCCATGGTGTTGAAGCGTCGAGCCGACTAGGGAACCTCCTTCCC-CGCCAGGATGGAA	2 TETETATGGTGGAGCGATETCACAGGCCTAGGACGTETCCTTTCCCTAGCGGGGATGGAC 61 182 GTGGCATCAGTCGCCGGCCTATTGCGCGGGCTGTTCTTCCCTGTGTTCTGCCGCCGCCGGCTGC 241	62 CTAACCGGGGTCGCCACCGCTTGCGGGGCCCTCTGGGCGGTCCGGTGCACTCGTTGC 121	242 CGCATTCGCTGCTCTCTGTGGCTTTTTCTGCTGAAGATCGGCCTGGAGCAGCGACG 301	302 CCACCGCTGGGCAAGACTCTGTAGGCTTCCTCCGAATCCCGTCGACTCCAGCC 361	GCTGAGCGCCGCGCCCTACCTGAGAGAAAAAGGAGATGGAGGCCGGGGACA	242 GAGCICUCUCUCUCUCUCAGAAACCCCCAAG-GAAAGAGAGACACAGGAACG 300 422 GGCGAICGCGGAAACGGCTICGGCCCTCGGCCTICCGGCCACCCTITITC 481	482 CCTCGGCGATCGCAAGCTCTTCTAAGTTCCCGAAGCCTCTTGGCCCGGAAAACTCC 541	GGGAACCCCACACTGCTTTCCTCTGCCCAGCCCGAGACTCGGGTCAGTTACTGGACGAAA	CIGCTCTCCCAAGCTCCTTGCGCCGCTCCCCGAATTGCTTCAAAAGTGCTAATTTGGAGCCTTAATTTGGAGCCTTTCAAAAGTGCTTAATTTGGAGCCTTTCAACTTTCAAGCTTGCTT	662 CAACTITICGGIGGAAIGTITCCGACCAGAIGGCIAGAITITIGCIGGAGICIACAGCGCC 721 	722 CTGAGAGCCCTGAAGGACGGGAGAAAACCAGCCCCCCACAGCGCAGAAATCTTTGAGT 781	782 TCGCTGCAGCTCGACCCCTCGGTCACCAGTCCCCTTGATTGGCTAGAGGAG 841	842 GGGATCCACTGGCCACACCCAGACCTAAAATTGGAGCTTAAGGCCAAGGGAAGT 901 	902 GCTTTGGACCCTGCAGCACAGGCTTTTCTCTTAGAGCAGCAGCAGGAGTGGAGCTG 961 	962 TTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTCGCCCTCT 1021		TCCTACCTGGACTGCTTCCTAGGCTAGAGAGTCAGCTGTGATGGAAATAGC	1142 GAGGTAGTCGGCTTCCAGACACTAACCCCAGAGCAGCTGCCTGAGAGACCATTGT 1201
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TCCAAAACTGCAGAGATAACCCAACACA 1441 CCCTGACCAGGATAATGGCTACCAGGCCTG 1381 TTCTGCCAGACCAGCTTGTAGTAACAACTG 1681 TCACCTTTGGAACTCTTTCTGCAGTGTAGAT 1861 TAGTICTGGGGAGGAAGATGACTGGGAATCT 2041 GTGGAACTCATTCTGTAATTCTGATGACCCC 2101 1989 2049 AGAAAGTGAATGTCCAGACTCGGTACAGCGT 2281 TCTTCGCATGAAACGGCTGGAATTCCTTCAA 1321 AAACACCCAGGAATCCACTGAAGAAAATA 1501 TGACCTGGAAACAAGTTCTGATCCAGAAGGT 1741 1572 AATTCAGACTGCTGCCAGAATTGTTCCTGAA 1921 2161 2221 recegerreregecaggarerecererr 1261 TTTGGAAGAGAGCCCTTCTGAGGGCTGT 1561 -------AGAGCCCCAGGGAAGCAGT 1392 GCCTGGAGGGCCGAATAAGTGTAGTTGAT 1621 TGGTTTTGATAGTGATAGCTCACTGTCAGAC 1801 TGGCAAGTCTGATCTAGAGAATTCCTCCCAG 1981 ICAAACATCAGGGGAAAATGAGAAAGGCTGT

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TGGAGCTGTTGCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTT 1013
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED" /note="lst strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                   GGGACTCCTATCCATGGTGTTGAAGCGTCGAGCCGACTAGGGAACCTCCTTCCCCGCCAG
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                                                                                                                                                                                                                                                                                           GGGACTCCTATCCATGGTGTTGAAGCGTCGAGCGACTAGGGAACCTCCTTCCCCGGCCAG
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                                                                                                                                    31.3%; Score 919.4; DB 1;
.larity 96.2%; Pred. No. 1.5e-247;
Conservative 14; Mismatches 22;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:31064080.
Contact: Genoscope
Control Satistic Structure of Sequence Sequence Season Cremically, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-loigo(dT) primer: Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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                          GAGGCTCTTGCTGGAGAAAGATACACCCATATCAAGAGAAAAAAGGTAACCTTCCTGGAA 2169
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AL526219 Homo sapiens NEUROBLASTOMA COT 25-NORWALIZED Homo sapiens
CDNA clone CSODCO16YI22 5-PRIME, mRNA sequence.
AL526219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 979)
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                                                                                                                                                                                GCAAGGGATGCATCCAGAAACGAATTCAAGAAACAGAAGTTGCCATTGGCTAC
                                                                                                    GAAGTTACTGAGTATTATATATAGTGGTGATGAGGATCGCAAAGGACCATGGGAAGAATTT
                                                                                                                                                                                                                                                                                                               GGACTTACTGTTGTACAGCAATGTTAAGAAGTGA-ACAGCCTGCAACCCGTGCCACTCT
                                                                                GAAGTTACTGAGTATTATATAAGTGGTGATGAGGATCGCAAAGGACCATGGGAAGAATTT
                                                                                                                                                                                                                                   TGCTTGACATTTGAACACAGAGAAGAATGTTTAATAGACTCCAGGGAACATGCTTCAAA
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/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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/db_xref="taxon:9606"
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KEYWORDS
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                           306 AGACTCTGTAGGCTTCCTCCGAATCCCGTCGACCTCCAGCCGCGGGCGCGGGCCCTA 365
                                                                                                                                              CCTGAGAGACTGTCAAGAAAAAGAGAGAGAGGGGGACAGGGGGATCGCGGAAACGGC 425
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B 1 (bases 1 to 897)

S NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Loading Aguality sequence stop: 673.
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/db_xref="taxon:9606"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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7939455 NIH MGC_67 Homo sapiens cDNA clone IMAGE:6172811
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908 TGGAGCTGTTGCCCAGTAGCCTTCAATCMCTGTCTGTTCTCTAACMGGGAMTTGGCTCTY 967
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_shape"
/note="Organ restis; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; Oligo-dT_primed.
Average insert size_2: S. Eb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                               DB 5; Length 873;
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                                                                                                                                                                                                                                                                                                                            Score 834.8; DB 5,
Pred. No. 1.2e-223
0; Mismatches 2;
/clone="IMAGE:6043767"
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Best Local Similarity 99.5%;
Matches 858; Conservative
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="texon:9606"
/db xref="texon:9606"
/clone="ImAGE:551220"
/tissue type="retinoblastoma"
/lab_hogt="bH10B (phage-resistant)"
/clone lib="NHH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Salie_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life Technologies."
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                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information action through the I.M.A.G.E. Consortium/Link at:
http://image.llh.gov
Plate: LLAM12264 row: j column: 21
High quality sequence stop: 599.
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                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
I (bases 1 to 1021)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z6.4%; Score 777.2; DB 4; Length 1021; Best Local Similarity 93.3%; Pred. No. 2.3e-207; Matches 889; Conservative 0; Mismatches 40;
                       sapiens (human)
                                              Homo sapiens
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TITLE
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AGENCOURT_6563011 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5551220
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and NotI enzymes and cloned into Sall/NotI site of pCMV-SPORT6 plasmid vector. The average insert size about 3.6kb."
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                                                                                                     Length 835,
                                                                                                                                           5; Indels
                                                                                                     Query Match 27.3%; Score 803; DB 6; L
Best Local Similarity 99.4%; Pred. No. 1.1e-214;
Matches 806; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1119 ATCAGAACAGTGATGGAAATAGCGAGGTAGT 1149
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BM559080
BM559080.1 GI:18802370
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: Ggabbe-r@mail.nih.gov
Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
CDNA Library Preparation: Yulan Piao and Minoru Ko
CDNA Library Preparation: Yulan Piao and Minoru Ko
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC C
can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM514 row: 1 column: 02
High quality sequence stop: 730.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD642687 L17-JUN-2003 AGENCOURT 14569880 NIA Human H1 Embryonic Stem Cell cDNA Library (Long) Homo Bapiens CDNA clone IMAGE:30427369 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2052 AAGCAG-AGAGTCTCAAACTGTGGAACTCATTCTGTAATTCTGATGA-----CCCCTACA 2105
                                                                                                                                                                                                                                 CTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCCTG-AAGAGCCTTCTGATTCAG 1937
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                                                                                                                                                                                                                                                                                                                                                                                                                    1998 AGA---CCCCTGAGCATAGTT-CTGGGGAGGAAGA--TGACTGGGAATCTAGTGCAGATG 2051
                                                                   CCCTGAAGGGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAA 660
                                                                                                                                                                                                                                                                                                                                                     AGAAGGATTTGTCTGGGCAGTCTGATCTAGAGAATTCCTCCCANTCTGGGAGCCTTCCNN 780
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//db xref="taxon:s606"
/db xref="taxon:s606"
/clone="IMAGE:30427369"
/tissue type="Embryonic Stem cells"
/cell lIne="WA01"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
                                                                                                                                                                                                                                                            CTTTACAGCAACAATTCAGACTGCTGCTGCAAATTGTTCCTGAAAGAGCCCTTCTGATTCAG 720
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AGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGATTGGGATGAGGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryoffa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (basea I to 775)
IIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                     CCCTGAAGGGCTTCACCTTTGGAACTCTTTCTGCAGTGTAGATCCTTATAATCCCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2106 ACCCTTTAAA---TTTTAAGGCTCCTTTTCAAACATCAGGGGAAAATGAGAAA 2155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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/organism="Homo sapiens"
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AUTHORS
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KEYWORDS
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CD642687
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COMMENT

ö Length 775; Indels Query Match 26.1%; Score 768.2; DB 6; Best Local Similarity 99.4%; Pred. No. 7.1e-205; Matches 770; Conservative 0; Mismatches 5;

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AGCGCCCTGAGGCCCTGAAGGGACGGGAGAAACCAGCCGCCCCCACAGCGCGCAGAAATCT 301 716

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420 835 480 895

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TTGAGTTCGCTGCAGCTCCTCAGACCCCTCGGTCACCAGTCCCCTTGATTGGCTA 361 176

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481 GAGGAGGGATCCACTGGCAATACTCGCCCCCAGACCTAAAATTGGAGCTTAAGGCCAAG 896 GGAAGTGCTTTGGACCCTGCAGCACAGGCTTTTCTCTTAGAGCAGCAGCTGTGGGGAGTG

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CA426770 1795 bp mRNA linear EST 07-NOV-2002 UI-H-FEI-bei-a-04-0-UI.sl NCI CGAP_FEI Homo sapiens cDNA clone UI-H-FEI-bei-a-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1690 TATTTTGGGAGGTGCATCCAGTGACCTGGAAACAAGTTCTGATCCAGAAGGTGAGGATTG 1749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCTTC 1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 TATTITGGGAGGIGCATCCAGIGACCTGGAAACAAGTICIGATCCAGAAGGIGAGGATG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 TCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCTTC 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 TGAAGCAGAGAGTCTCAAACTGTGGAACTCATTCTGTAATTCTGATGACCCCTACAACCC 254
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bummalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 795)
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                                                                                                                                                                                                                                                                          1570 TGAGATACCTATGGAAAGGAGCCTGGAGGGCCGAATAAGTGTAGTTGATTACTCATA
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                                                                                                                Length 793;
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                                                                                                                    Score 758; DB 6; I
Pred. No. 5.5e-202;
                                                                                                                                                                                               0; Mismatches
TAG_SEQ=CGCTACGGAC"
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                                                                                                                25.8%;
ilarity 99.1%;
Conservative
                                                                                                                                                              Similarity
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Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 793)

SICI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Upublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Martin

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento-Soares university of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, Dento-soares@dulowa.edu

The following repetitive elements were found in this CDNA sequence: 1-22, AAT_rich#Low_complexity

Seq primer: N13 FORWARD

POLYA=YES.
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//un.xerier.uson.rough
//usoue_type="cell lines"
//dev_taige="cell lines"
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                                                                                                                                                                      601 GAGCTGTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTCG 660
GAGCTGTTGCCCAGTAGCCTTCAATCCCGTCTGTACTCTAACCGGGAACTTGGCTCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1076 AACCCTTCCTACCTGGACTGCTTTCCTAGGCTAGAAGTCAGCTATCAGAACAGTG 1130
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens
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495 AATCCCCAGAACTTTACAGCAACAATTCAGACTGCTGCCAGAATTGTTCCTGAAGAGCCT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 CCTTTAAATTTTTAAGGCTCCTTTTCAAACATCAGGGAAAATGAGAAAGGCTGTCGTGAC 196
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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602698720F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4830749 5',
                                                                                                                  375 AGCCTTCCTGAGACCCCTGAGCATAGTTCTGGGGAGGAAGATGACTGGGAATCTAGTGCA
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                                                                              1928 TCTGATTCAGAGAAGGATTTGTCTGGCAAGTCTGATCTAGAGAATTCCTCCCAGTCTGGA
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// woll types-mRNAm
/ db xref="taxon:9606"
/ clone="UT-FE1-bei-a-04-0-UI"
/ tissue type="Cell lines"
/ dev_stage="Adult"
/ lab.host="Bhl108 (Life Technologies)"
/ lab.host="Bhl108 (Life Technologies)"
/ clone lib="NCI CGAP FE1"
/ note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP FE1 is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo. Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector: The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
edynamic result in the University of Iowa.
TAG TISUE-Human grade 2 chondrosarcoma cell line pool
                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CONA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-goareseniowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-22, AT rich#Low_complexity
BOUNA=Yes.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Pred. No. 2.6e-201;
0; Mismatches 9; Indels 0
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TAG_SEQ=CGCTACGGAC"
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Best Local Similarity 98.8%;
Matches 761; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIFMI/NHGRI, National Institutes of Health). Note: this a NIH MGC Library."
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                                                                     Length 850;
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                                                                   Score 748.8; DB 4;
Pred. No. 2.2e-199;
0; Mismatches 12;
                                                                  tch 25.5%;
cal Similarity 97.9%;
811; Conservative (
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ISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Enamia; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 875)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Intublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapba remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13494 row: p column: 13

High quality sequence stop: 557.

ES 1. Constinn(Vualifiers)
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/tismue type="retinoblastoma"
/tismue type="retinoblastoma"
/clone_lib="UH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: eye; Vector pCMV-SPORT6; Site_1:
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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CATTGTGGCCATTTCTGAGTGTCACACCTTACTTTCTTGTAAGGTGCAGCTGTTGGGGAG 2247

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BQ427697

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AGENCOURT 7898324 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6154236

S, mRNA sequence.

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LOCUS DEFINITION RESULT 13

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ACCESSION

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CB989883 13903499 NIH MGC_147 Homo sapiens cDNA clone IMAGE:30341796 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
E 1 (Bases I to 838)
I Lobases I to 838)
I Mational Institutes of Health, Mammalian Gene Collection (MGC)
I Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carniaci (RIKEN)
cDNA Library Arrayed by: The I M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: NDAM613 row: i column: 11
High quality sequence stop: 595.
Location/Qualifiers
I Location/Qualifiers
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AGENCOURT 15624090 NIH MGC 147 Homo sapiens cDNA clone
IMAGE:30528106 5', mRNA sequence.
CF594071
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ACATGTCNAAAGAAAAAAGGTAACCTTCCTTGAAGAAGTTACTGAGTATTATATAAAGTGG
                                                                       AG--AATGTTTAATAGACTCCAGGGAA 2510
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1.E 1 (bases 1 to 793)

1.S NH-WGC http://mgc.nci.nih.gov/.

1.National Institutes of Health, Mammalian Gene Collection (MGC)

1.National Institutes of Health, Mammalian Gene Collection (MGC)

1.National Institutes of Health, Mammalian Gene Collection (MGC)

1.National Institutes of Health, Mammalian Gene Collection

1.National Institutes of Health, Mammalian Gene Context: Robert Englished Tissue Procurement: Dr. Stefan Hansson

1.National Email: Gapba-rémail.nih.gov

1.National Library Preparation: Michell Brownstein (MHGRI) with help

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 793)
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               WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN
                              181 WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLCFPRLEVSYQN
                                                                                                                                                                                                                                       CSNXLIDYILGGASSDLETSSDPEGEDWDERAEDDGFDSDSSLSDSDLEQDPRGLHLWNS
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                                                                SDGNSEVVGPQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR
                                                                                  SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR
                                                                                                                    LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES
                                                                                                                                   LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPXHCRDNPTQFVPAAGDIPGNTQES
                                                                                                                                                                        TEEKI ELLTTEVPLALEEESPSEGCPSSEI PMEKEPGEGRI SVVDYSYLEGDLPI SARPA
                                                                                                                                                                                                                         CSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNS
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A, Nagai K
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T, Wakamatsu
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
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Sugiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening test substances for preventing or treating disease involving oxidative stress, by testing test substances for its ability to inhibit activity of GADD34L and identifying test substance that inhibits activity of GADD34L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of screening several test substances for preventing or treating diseases involving oxidative stress such as neuronal ischaemia, heart ischaemia, renal damage induced by ischaemia or toxins, autoimmune diseases and neurodegenerative disorders. The method involves testing the test substances for its ability to inhibit the activity of GADD34-like (GADD341), also referred to as eIF2alpha-specific regulatory subunit of phosphatase, and identifying the sequence which inhibites the activity of GADD34L. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTA 120
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Novel
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                                                                                                                                                                                                                        Oxidative stress, neuronal ischaemia; heart ischaemia; renal damage; autoimmune disease; neurodegenerative disorder; therapy; GADD34-like; GADD34L; eIF2alpha-specific regulatory subunit; phosphatase; human.
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100.0%; Pred. No. 7.5e-303;
tive 0; Mismatches 0;
                                                     ALIGNMENTS
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ADR09563
ABG22101
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                                                                                                                    ADQ88458 standard; protein; 713
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                                                                                                                                                                                               Human GADD34-like (GADD34L)
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N-PSDB; ADQ88457.
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Local Si.
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprises one of the 5602
complementary strand of a polynucleotide which comprises one of the 5602
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide opprises at least 15 nucleotides and the combination of
the 5'-end sequence[3'-end sequence] selected from those defined in the
gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
converse of detection and/or diagnosis of the abnormality of the full-length
cDNAs easily without any specialised methods. AAH13612 represent
ceptesent human amino acid sequences; and AAH13622 to AAH13612
ceptesent human amino acid sequences; and AAH13622 trepresent
ceptesent human amino acid sequences; and AAH13622 trepresent
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                        8; SEQ ID NO 18965; 2537pp + Sequence Listing; English.
                                                                                           Claim
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Sequence 713 AA;

ö WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDDFSVVSYLLNDSYLDCFPRLEVSYQN 240 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR 300 CSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNS 480 540 DDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISE 600 541 DDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISE 600 SYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTA 120 SYWTKILSQLIAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTA 120 QKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQL 180 WGVELLPSSLOSRLYSNRELGSSPSGPLNIORIDNFSVVSYLLNPSYLDCFPRLEVSYQN 240 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR 300 LEFLOQANKGODLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES 360 LEFLOGASKGODLPTPDODNGYHSLEEEHSLLRMDPKHCRDNPTOFVPAAGDIPGNTOES 360 TEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPA 420 TEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPA 420 CSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNS 480 1 MEPGTGGSRKRLGPRAGFRFWPPFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV 60 1 MEPGIGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPIPLGPENSGNPILLSSAQPEIRV 60 FCSVDPYNPONFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEE PCSVDPYNPQNFTAT1QTAAR1VPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEE Gaps ö Score 3794; DB 4; Length 713; Pred. No. 5e-302; 2; Mismatches 0; Indels C 99.7%; Conservative Query Match Best Local Similarity Matches 711; Conserv 361 421 301 61 181 241 241 361 481 481 63 121 121 301 421 유 ठे g ò 셤 ઠે 셤 ð ద ે 셤 ઠે 용 ò 셤 ሯ

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95.3%; Score 3627; DB 3; 98.8%; Pred. No. 2.5e-288; iive 1; Mismatches 7;

Conservative

Best Local Similarity Matches 683; Conserv

Sequence 707 AA;

Length 707;

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called human colon cancer antigens, given in AAB5234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynuclectides, core be used in gene therapy. The colon cancer antigen polynuclectides, treatment and antibacies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynuclectides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, gastrointestinal cardiovascular disorders, AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present invention
      601 CHTLLSCKVOLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
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                                                                                                                                                                                                                                                                                                                                                                identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                           713
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                                                                                                                                                                                                                                                                                                                                               colon cancer; colon cancer antigen; diagnosis; detection;
                                                                    PWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQGTCFKGLNVLKQC
                                                                                                                                                                                                                                                                                                        Human colon cancer antigen protein sequence SEQ ID NO:941.
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                                                                                                                                                                                    AAB53401 standard; protein; 707
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PPPPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKVL
                             IWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSPLDW
                                    LEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGS
                                                                   SPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLRE
                                                                                                SPSGLLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLRE
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                                                                                                                                                                                                                                                                               DDPYNPLNPKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidative stress; neuronal ischaemia; heart ischaemia; renal damage; autoimmune disease; neurodegenerative disorder; therapy; GADD34-like; GADD34L; eIF2alpha-specific regulatory subunit; phosphatase; mouse.
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g test substances for preventing or treating disease involving e stress, by testing test substances for its ability to inhibit of GADD34L and identifying test substance that inhibits activity
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                                                                                                                                                                                                                                                                                                  The present invention relates to a method of screening several test substances for preventing or treating diseases involving oxidative stress such as neuronal ischaemia, heart ischaemia, renal damage induced by ischaemia or toxins, autoimmune diseases and neurodegenerative disorders. The method involves testing the test substances for its ability to inhibit the activity of GADD34-like (GADD34L), also referred to as elfalpha-specific regulatory subunit of phosphatase, and identifying the sets substance which inhibits the activity of GADD34L. The present sequence is the mouse GADD34L protein.
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| OKSLSYTAAGLFAKTRVVSTLALARGGTPVAVLVJLRLEVKLKAQERALDSAAPTFILEQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OKSLSSLQLD-SSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEPGTGGSRKKLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEEKIBLLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARP
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                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 4; 30pp; English
                                                                                                    2004-552556/53
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                                                                                                                         N-PSDB; ADQ88459
                                                                                                                                                               Screening test s oxidative stress activity of GADD of GADD34L.
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                                                                                                                                                                                                                                                                                                                                                               Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
antific ammentory; antirheumatic; antiarthritic; immunosupressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; central nervous system; virucide;
antibacterial; endocrine; cardiant; cardiavascular; antianaemic; anaemic;
antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antidapressant; nootropic; antidiabetic; cytostatic;
neuroprotective; antidapressant; nootropic; antidiabetic; cytostatic;
munopotective; antidapressant; nootropic; antidiaren; inflammation;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylactic; rheumatolid arthritis; septic shock; pancreatitis;
cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
genetic disease; haematopoietic disorder; platelet disorder; asthma;
thrombocytopaenia; osteopororasis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
allergic rhinitis; disbetes; multiple sclerosis; depression;
antibalmer's disease; Parkinson's disease; neurodegenerative disorder;
584 GHHTLLSCKAQLLESQEDNCPGCGLGEALAGERYTHIKRKKVTFLEEVTEYYISGDEDRK 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                    GPWEEFARDGCRFOKRIQETEVAIGYCLAFEHREKMFNRLR 684
                                           GPWEEFARDGCRFOKRIOETEDAIGYCLTFEHRERMFNRLQ 700
                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:963.
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                                                                                                                                                                                              AAM25448 standard; protein; 153
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25-APR-2000; 2000US-00552317.
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                                                                                                                                                                                                                              623
                                                                                                                                                                                                                                                                                                     683
                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                  63
anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, parkinson's disease, neurodegenerative and neurological disorders
                                                                                                                                                                                                                              564 DPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSV
                                                                                                                                                                                                                                                      4 DPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSV
                                                                                                                                                                                                                                                                                                       624 ORDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFOKRIQETEDAI
                                                                                                                                                                                                                                                                                                                           QRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGFWEEFARDGCRFQKRIQETEDAI
                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, apoptosis associated protein; GADD34; antiviral agent; growth arrest and DNA damage-inducible gene 34; viral infection; serine/threonine phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening assay for potential antiviral agents that modify serine/threonine phosphatase activity for treating human viral
                                                                                                                                                   Length 153;
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                                                                                                                                                     Score 813; DB 4; I
Pred. No. 2.8e-58;
                                                                                                                                         21.4%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                GYCLTFEHRERMFNRLQGTCFKGLNVLKQC 713
                                                                                                                                                                                                                                                                                                                                                                                                      124 GYCLTFEHRERMFNRLOGTCFKGLNVLKOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                           Matches 150; Conservative
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N-PSDB; AAZ99766.
                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                  Sequence 153 AA
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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GENBANK; XP_009097.
                                            Homo
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                                                                                                                                                                                                      78 RPEEEAEDSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                         167 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                       134 FADGQRAPL----SPSLLIRTLQGSDKNPGEEKAEEEGVAEEEGVNKFS-----YPPS 182
                                                                                                                                                                                                                                                                                                 227 YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
                                                                                                                                                                                                                                                                                                                                                         STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
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                                                                                                    Gaps
activation of a host-cell interferon-induced, double-stranded RNA-activated protein kinase e.g. P68, eIF2 or eIF2alpha
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                                                                      Length 674;
                                                                                                 Indels
                                                                                                                             LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR-
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                                                                      DB 3;
                                                                     tch 6.8%; Score 260.5; DB 3; al Similarity 21.9%; Pred. No. 6.3e-12; 164; Conservative 80; Mismatches 263;
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Costigan M;

Befort K,

Woolf C, D'urso D,

(GEHO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

14-AUG-2002; 2002WO-US025765.

WO2003016475-A2 27-FEB-2003

The invention discusses a composition comprising two or more isolated factor the invention discusses a composition of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also calaimed are a vector comprising the novel polywuclectide, a method for identifying a nagent that is differentially regulated in an animal subjected to pain and a stray, a method for identifying a nagent that is differentially expression of the polymuclectide sequence that is differentially expression of the polymuclectide sequence that is differentially expression of a polymuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymuclectides, a method for more of the polymuclectides, a method for identifying a compound useful in treating cativity in an animal of one or more of the polympetides or their antibodies. The polymuclectide or the compound to the sequence utical composition comprising the one or more polympetides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain in trate or pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the sequence data for this patent did not form part of the printed the sequence data for this adifferentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed security in the sequence data for this patent did not form attently from WIPO at the contract of the printed security in the sequence data for this patent did not form attently from wIPO at the contract of the sequence data for this patent did not form attently from wIPO at the contract of t LLSPVMGLLSRA--WSRL-RGLGPLEPWLVEAVKGAALVEAGLEGEARTPLAIPHTPWGR -----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA Length 674; LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR--Indels a composition comprising two 6.8%; Score 260.5; DB 7; Local Similarity 21.9%; Pred. No. 6.3e-12; Les 164; Conservative 80; Mismatches 263; ftp.wipo.int/pub/published pct sequences Claim 1; Page; 1017pp; English. invention discloses Sequence 674 AA; 21 113 Query Match 셤 Š 요 ò 셤 ઠે

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166
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                                                                                                                                         167 LDPAAQAFILLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
77
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Human; pain; neuronal tissue; gene therapy;

Human Protein XP_009097, SEQ ID NO 553.

(first entry)

29-JAN-2004

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ADE54748

ADE54748 standard; protein; 674 AA

RESULT 7 ADE54748

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YLDCPPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
            STEGLPRIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
                                                         ---GEEENQATEDKRTERSKGARK--------TSVSPRSSGSDPRS 259
                                                                                                                                      -----ALGAAEKDGEAECPPCIPPPSAFLKAWVY 344
                                                                                                                                                          444 -EGEDWDEEAEDDGFDSDSSLSDSDLEQDPEG-----LHLWNSFCSVDPYNPQNF 492
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                                                                                                                                                                                                                  ----SSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPPQTSG-----ENEKG 584
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spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                   EGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDP-
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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WPI; 2003-268312/26.

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

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Claim 1; Page; 1017pp; English.

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Claim 1; Page; 1017pp; English.

XX

The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the noval polymucleotide sequence. Also claimed are a vector comprising the noval polymucleotide sequence. Also claimed are a vector comprising the properties of the noval polymucleotide sequence which is differentially regulated in an animal subjected to pain an expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotide sequence which is differentially expressed in an enthod for identifying a compound that regulates the activity of one or more of the polymucleotides a method for pain, a method for pain, a method for identifying a compound which regulates the activity of one or more of the polymelestics and method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the polymelestics and spated nerve injury (SNI) in an animal (Solution and appared one or more of the polymelestics one or more of the sequence data for this patent did not form part of the grain of the printed spatent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly form part of the printed in electronic form part of the printed in electronic form part of the printed in electr
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Ouery Match 6.8%; Score 260.5; DB 7; Best Local Similarity 21.9%; Pred. No. 6.3e-12; Matches 164; Conservative 80; Mismatches 263;

32;

241; Gaps

Length 674; Indels 241

396

344

444 - EGEDWDEEAEDDGFDSDSSLSDSDLEQDPEG-----LHLWNSFCSVDPYNPQNF 492

345 WPGEDTEEE-EDEEEDEDSDSGSDEEEGEARASSSTPATGVFLKSW-----VYQPGED

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The invention discloses a composition comprising two or more isolated rat derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic animal subjected to palan and a which is differentially regulated in an animal subjected to palan and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a plint animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a
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                                                                                                                                                                     -----YVPGEKPPPWAPPRLPLRLORRLKRPETPTHD
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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TATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP-
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that molympeptides or their antibodies. The polymucleotide or the compound that polympeptides or their antibodies. The polymucleotide or the compound that pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (Ct) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPEEEAEDSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEBEHSLLRMDPKHCRDNPTQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GEEENQATEDKRTERSKGARK--------TSVSPRSSGSDPRS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSG-----ENEKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 HRECCPAVE---EEDD------EEAVKKBAHRISTSALSPGSKPSTWVSCP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP-------ETPEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRD--SKTPSESIVAISECHTLLSCKVQLLGSQ-----ESECPDSVQRDVLSGGRHTH-
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                  Length 674;
compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               70 LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR-
                                                                                                                                                                                                                                                                                                                                                6.8%; Score 260.5; DB 7;
21.9%; Pred. No. 6.3e-12;
ve 80; Mismatches 263;
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                                                                                                                                                                                                                                                                                                                                                                    21.9%;
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 21.9%
Matches 164; Conservative
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605 PCLTPAARARARIRNPPLAPIPALTO 632

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The present interaction describes primer abers 10.0 syntheorising present interaction describes primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the polynucleotide comprises a 1'-end sequence, where the polynucleotide comprises a 1'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer set useful for synthesising polynucleotides, the full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH13618 co AAH13628 represent human amino acid sequences; AAB93446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13622 represent the second of the exemplification of the constant of the constant and any appearance of the constant and any sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 11494; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi K, Saito K, Ye
A, Nagai K, Otsuki T;
                                                                                                                           Human protein sequence SEQ ID NO:11494
AAB92888 standard; protein; 674 AA
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Sugiyama T, Wakamats
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02-MAY-2000; 2000JP-00118776.
                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                 99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-2000; 2000JP-00241899
                                                                               (first entry)
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                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                               07-FEB-2001.
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Ishii S,
                                     AAB92888;
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488
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                                                                                                                                                                                                                                                                                                                                                                                            SEG WEYRSG-----EASEEKEE-----KAHEETGKGEAAPGPQSSAPAQRPQLKSWWCQ 305
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                                                                                                                                                                                                                                                                                                                                                                  346 FVPAAGDIPGNTQESTEEKIELLTTEVPLALEESSPSEGC--PSSEIPMEK-----E 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 PSDEEESEV------KP----KP----LGAAEKDGEAECPPCIPPPSAFLKAW 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 BDT------EEEEDEDSDTGSAEDEREAETSASTPPASAFLKAWVYRPGEDTEEE 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 VYWPGEDTEEE-EDEEEDEDSDSGSDEEEGEAEASSSTPATGVFLKSW-----VYQPG 394
21 LLSPVMGLLSRA--WSRL-RGLGPLEPWLVEAVKGAALVEAGLEGEARTPLAIPHTPWGR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA
                                                                                                                      67 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS
                                                                                                                                                            134 FADGQRAPL----SPSLLIRTLQGSDKNPGEEKAEEEGVAEEEGVNKFS----YPPS
                                                                                                                                                                                                                                          183 HRECCPAVE---EEDD------EEAVKKEAHRTSTSALSPGSKPSTWVSCP--
                                                                                                                                                                                                                                                                                                                          ---GEBENQATEDKRTERSKGARK-------TSVSPRSSGSDPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDP-
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34; .--- 112

Gaps

237;

1. 6.8%; Score 259.5; DB 4; Length 674; Similarity 22.3%; Pred. No. 7.7e-12; Conservative 82; Mismatches 261; Indels 237

LLAPLPGLLOKVLIWSQLFGGMPPTR-WLDPAGVYSAL--RALKGR--

2

Matches 166, Conservative

Query Match Local ---- YPPS 182

443

589

-----ETPEH 535

635

989

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STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
                                                                                                                                                                                                                                                                                 FVPAAGDIPGNTQESTEEKIELLTTEVPLALEESPSEGC--PSSEIPMEK-----E 395
                                                                                                                              ---EEDD-----EEAVKKEAHRTSTSALSPGSKPSTWVSCP-- 224
                                                                                                                                                                                                                                 ---TSVSPRSSGSDPRS 259
                                                                                                                                                                                                                                                                                                                                   WEYRSG-----EASEEKEE-----KAHEETGKGEAAPGPQSSAPAQRPQLKSWWCQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KP-----KP-----LGAAEKDGEAECPPCIPPPSAFLKAW 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LHLWNSFCSVDPYNPQ 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 ETEEEBAAEDWGEAEPCPFRVA--IYVPGEKPPPWAPPRLPLRLQRRLKRPETPTHDPD 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 PETPLKARKVRFSEKVTVHFLAVWAGPAQAARQGPWEQLARDRSRFARRIAQAQEELSPC 606
                                                                              YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL
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PGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 NFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EGEDWDEBAEDDGFDSDSSLSDSDLEQDPEG-----
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                                                                                                                                                                                                                               ---GEEENQATEDKRTERSKGARK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW99891 standard; protein; 674
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                                                                                                                              183 HRECCPAVE-
                                                                                                                                                                                                                                                                                                                                                                                                                                      PSDEESEV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW99891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to the novel association of protein sequences (and the genes which encode them) to the NP-kappaB pathway. The invention may be useful for the production of compounds with an antininflammatory, cytostatic, hepatotropic, virucide, antiarteriosclerotic, antiarteriosclerotic, gastrointestinal-Gen, antiathmatic, antiarteriosclerotic, carebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NP-kappaB pathway. The condition is an immune disorder, an inflammatory disorder.

CC useful for aberrant NP-kappaB requiation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM credermal dysplasia, X-linked anhidrotic ectodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, inflammatory viral infections, HIV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell cetodermal dysplasia, inflammatory disorders colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, BAE, autoimmune adsorders related to aberrant acute phase responses, cyperongenital conditions, birth defects, necrotic lesions, wounds, cygan transplant rejection, conditions related to organ transplant corresponders related to aberrant signal transduction, cygan transplant rejection, conditions related to organ transplant cyferion, conditions related to organ transplant cyferiating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human protein which as a bubject to the novel association with the NP-kappaB pathway of the inventive by the index of the invention but appear in the specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 RPGEEAEDSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                          aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; HIV propagation; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LLSPVMGLLSRA--WSRL-RGLGPLEPWLVEAVKGAALVEAGLEGEARTPLAIPHTPWGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 259.5; DB 8; Length 674; 22.3%; Pred. No. 7.7e-12; ive 82; Mismatches 261; Indels 237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained by the indexer from Genbank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; SEQ ID NO 90; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feder JN,
  autoimmune disorder; hyper immune
                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                          2003US-0440068P.
2003US-0469757P.
                                                                                                                                                                                                                                                                                                           13-JAN-2004; 2004WO-US000798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nadler SG, Neubauer MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-562168/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 674 AA;
                                                                                                                                                                                                          WO2004065577-A2
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          14-JAN-2003;
12-MAY-2003;
                                                                                                                                                                                                                                                            05-AUG-2004
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The present sequence represents a human growth regulator protein, designated GRREG. The protein can be used in methods to treat cancer. The protein can also be used in binding assays to detect (ant) agonists of GRREG. A fragment from the nucleic acid sequence encoding GRREG can be used as a probe for detecting GRREG encoding sequences (especially in PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586
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                                                                                                                                                                                                                                                                                                                                                                              -----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLDCPPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRECCPAVE---EEDD------EEAVKKEAHRISISALSPGSKPSTWVSCP-- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TSVSPRSSGSDPRS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 YSYLEGDLPISARPACSNKLIDY------ILGGASSDLETSSDP----- 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PQSSAPAORPQLKSWWCOPSDEEESEVKALGAAEKDGEAECPPCIPPPSAFL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DPHP----SHPDQSAHFRGWGYR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RPEBEAEDSGGPGEDRETLGLKTSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 PADGQRAPL----SPSLLIRTLQGSDKNPGEEKAEEEGVAEEEGVNKFS----YPPS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----EGEDWDEEAEDDGFDSDSSLSDSDLEQDPEG------LHLWNSFCSVDPY 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKETEEBEBAEDWGEAEPCPFRVA--IYVPGEKPPPWAPPRLFLRLQRRLKRPETPTH
                                                                                                                                                                                                                                                                                                                               FVPAAGDI PGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 PEH-----SSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSKTPSESIVA----ISECHTLLSCKVQLLGSQ-----ESECPDSVQRDVLSGGRHTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFOKRIQETEDAI
                                                                                                                                                                                                                                                                                                          70 LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPGEDT------EBEEDEDSDTGSAEDEREAETSASTPPASAFLKAWVYRPGEDT
Novel human growth regulator protein - useful in the treatment of
                                                                                                                                                                                                                                         Length 674;
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                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                      6.6%; Score 252.5; DB 2;
21.9%; Pred. No. 2.9e-11;
tive 80; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYCLTPEHRERMFNRLQGTCFKGLNVLKQ 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 EEEEDEDVDSEDKEDDSEAALGEAES
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                                                Fig 1; 70pp; English
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                        Sequence 674 AA;
                                                                                                                                                                                                                                                                        164;
                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 164
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                                                  Claim 1;
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RESULT 13 AAY41102

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The invention relates to an inducible progression-elevated gene-3 (PEG-3 gene) regulatory region functionally linked to a gene encoding a product that causes or may be induced to cause the death or inhibition of cancer cell growth. A vector of the invention which contains a gene encoding thymidine kinase or a product which causes the cell to express a specific antigen can be administered along with gancyclovir or acyclovir, or an antiged, or fragment to the antigen, respectively, to treat cancer in a subject. The PEG-3 gene is useful for generating new cloning and expression vectors, transfected cells, and for developing methods for cultured growth of such cells. The PEG-3 polymucleotide is also useful as a source of primers and probes to study the progression of cancer, and to detect the presence of the gene. The present sequence represents the amino acid sequence of the rat MyDl16 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 REKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIHHLRMKRLEFLQQANKG---QDLPTPDQDNGYHSLEEEHSLLR------MDPKHCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSS--EIPMEKEPGE
                                                                                                                                region; cell
acyclovir; ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALLITPTPVSG-NLLP-----HGETEESGSPEQSQAAQRL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel vectors useful for studying the progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPRPO-HVLHWRDAHNFYLLSPLMGLLSRA--WSRLRGPEVPEAWL-
                                                                                                                                Progression-elevated gene-3; PEG-3 gene; regulatory cell growth; cancer; thymidine kinase; gancyclovir; MyD116 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 238; DB 2; L, Pred. No. 4.3e-10; 81; Mismatches 233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%; Score 238; 22.4%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 3A-B; 251pp; English.
AAY41102 standard, protein, 657
                                                                                                                                                                                                                                                                                                                                                                        COLUMBIA NEW YORK.
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                                                                                                Rat MyD116 protein sequence
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Matches 173; Conservative
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199 STPVPFLGEA----EHQATEEK----GTE-NKADPSNSPSSGSHSRAWEYYSREKPKQ
                                                                                              :: | | | | :: | | | | EE---NSDLDSAEEDTAQTGATPHTSPFLKAWVYRPGEDTEDDTEEEEDSENVAPGDSET
                                                                                                                                                                                                                                                                                           PKLPLRLQRRLRLFKAPTRDQDPEIP-----LKARKVHFAEKVTVHFLAV
                                                          -----EGEAKVEÁHRÁGOGHPCRNAEAEE--GGPETTFVCTGNAFLKAWVYRPG
                                                                                   ----GFDSDSSLSDSD-LEQDPEGL-
                                                                                                                                 ------ATIQTAARI----VPEEPSDSE
                                                                                                                                                         ATPHT-SAFLKAWVYRPGEDTEEENSDLDSAEEDTAQTGATPHTSAFLKAWVYRPGEDTE
                                                                                                                                                                               KDLSGKSDL----ENSSQSGSLPET------PEHSSGEEDDWES----S
                                                                                                                                                                                                                               ADEAESLKLWNSFC-----NSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAI
                                                                                                                                                                                                                                              || ::| | | | | | | | ADSSQSPCLQPQRCLPGEKTKGRGEEP--PL-FQVAFYLPGEK------PESPWAA
                                                                                                                                                                                                                                                                             SECHTLLSCKVQLLGS----QESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse ischaemic condition related protein sequence SEQ ID NO:1062
                                                                                                                                                                                                                                                                                                                            700
                                                                                                                                                                                                                                                                                                                                        vasospastic ischaemia; ischaemic condition; ischaemic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ischaemia;
                                                                                                                                                                                                                                                                                                                           ----GDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ
                                    GRISVVDYSYLEGDLPISARPA-----CSNKLIDYILGGASSDLETSSDP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compressive ischaemia; occlusive
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                                                                                                                                ---HLWNSFCSVDPYNPQNFT----
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                                                                                  EDWDEE----AEDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                            ABB57373 standard; protein;
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N-PSDB; ABI99909.
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is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in AB877020 to ABB57314) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KRLGEVVAREEGVAEPAYPTSQLEGGPAENEEDGETVKTYQASAASIAPGYKP 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSS--EIPMEKEPGE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STPVPFLGEA-----EHQATEEK----GTE-NKADPSNSPSSGSHSRAWEYYSREKPKQ 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 TEEEDNSDSDSAEEDTAQTGATPHTSAFLKAWVYRPGEDTEEE-----DSDSDSAEEDT 350
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                                                                                                                                                                                                                                                                                                                  SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCF
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                                                                                                                                                                                                                                                                              292;
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                                                                                                                                                                                                                                          Length 657;
                                                                                                                                                                                                                                        Query Match 6.2%; Score 237; DB 5; Length 65° Best Local Similarity 21.8%; Pred. No. 5.2e-10; Matches 169; Conservative 81; Mismatches 233; Indels
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AAW79958 standard; protein; 578

RESULT 15 AAW79958 ID AAW7

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method

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This polypeptide comprises human progression elevated gene-3 (PEG-3) protein. The amino acid sequence was deduced from an isolated cDNA clone (see AAV65765). PEG-3 expression (1.5 and 2.8 kb transcripts) is elevated in most human tumour cell lines. The amount of PEG-3 in a cell is also an indicator of DNA damage in that cell. Cells in which a reporter gene in indicator of DNA damage in that cell. Cells in which a reporter gene in control of the promoter or regulatory region (see AAV65766) of the rat PEG-3 gene can be used in methods for identifying agents that modulate PEP-3 expression or the ability of PEG-3 to induce progression, or for determining whether an agent is capable of inhibiting DNA damage and repair pathways, cancer progression or oncogene-mediated rannals and repair pathways, cancer progression or oncogene-mediated and ammals and vaccines comprising PEG-3 pulypeptides and an immune response enhancer are also claimed. Antibodies (especially monoclonal) to the PEG-3 may be used to determine tumour progression of a cells can be protected from chemotherapeutic damage by inhibiting or eliminating the expression of PEG-3 in the cells The methods can be applied to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumorigenesis, angiogenesis or metastasis, to melanoma, brain, cervical, prostate, lung or colorectal cancer, neuroblastoma or glioblastoma (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Progression Elevated Gene-3 - used to develop products foe.g. modulating DNA damage and repair pathways, cancer progression or oncogene mediated transformation and angiogenesis
                                                                                                                                                              DNA repiar; tumorigenesis; angiogenesis; metastasis; melanoma;
brain cancer; cervix cancer; prostate cancer; lung cancer;
colorectal cancer; neuroblastoma; glioblastoma; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWL--DFAGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                progression phenotype comprising anchorage-independent growth,
                                                                                                                                        Progression elevated gene-3; PEG-3; human; tumour progression;
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21.7%; Pred. No. 1.3e-08;
tive 79; Mismatches 223; Indels 2
                                                                                                  Human progression elevated gene-2 (PEG-3) protein.
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70 LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR------ 112
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Best Local Similarity 21.9%; Pred. No. 9.1e-13;
Matches 164; Conservative 80; Mismatches 262; Indels 243; Gaps
                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Puri
APPLICANT: Shah, Puri
MUNGER OF SEQUENCES:
APPLICANT: Shah, Puri
APPLICANT: All A Porter Pharmaceuticals, Inc.
STREES: Incyte Pharmaceuticals, Inc.
STREES: ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: ACA
COUNTRY: USA
APPLICANT USA
COMPUTER READBLE FORM:
MUSTER: Ind. Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Faled Herewith
APPLICATION NUMBER:
Filing DATE:
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 37,749
REFERENCE/DOCKET NUMBER: 37,749
REFERENCE/DOCKET NUMBER: 37,749

ALIGNMENTS
                                                                                                                                                                        Sequence 1, Application US/08893852A Patent No. 6080558 GENERAL INFORMATION:
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225 -	346 F	260 %		288 -		340 F	488 N	392 (533 E	441 E	1 783	486 E	- 989	544 I	684 0	604 8	RESULT 2 US-08-093-852A-3 US-08-093-852A-3 Sequence 3, Applicat: Patent No. 6080558 GENERAL INFORMATION APPLICANT: Lal, APPLICANT: ON APPLICANTION APPLICANTER: LBM COMPUTER: LBM APPLICANTION APPLICANTION APPLICANTION APPLICANTION APPLICATION NUM FILING DATE: FILING DATE: ATTORNEY/AGENT IN APPLICATION NUM REFERENCE/DOCKET TELECHONE: TELECHONE: TELECHONE: 415:	TELEFAX: 4 INFORMATION FOR
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IDENTIFICATION OF THE PROGRESSION ELEVATED GENE-3 AND USES THEREOF
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NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 657 amino acids
amino acid
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Matches 165; Conservative
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                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
   INVENTION:
 TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
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                                                                                                                                                10036
                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                  53 SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKG 111
                                                                                                                                                                                                                                                                                                 112 REKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAA 171
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                                                                                                                                                               6.2%; Score 237; DB 3; Length 657;
Similarity 21.8%; Pred. No. 1.9e-11;
59; Conservative 81; Mismatches 233; Indels 292;
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               i LENGTH: 657 amino acida

TYPR: amino acida

TYPR: amino acida

TYPR: amino acida

STRANDEDNESS: eingle

TOPOLOGY: linear

INMEDIATE SOURCE:

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ICLONE: 53041
                                                                                                                                                                                                 Matches 169; Conservative
     SEQUENCE CHARACTERISTICS
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Sequence 3, Application US/08821818 Patent No. 6146877 GENERAL INFORMATION: APPLICANT: Fisher, Paul B.

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157 GVAEPAYPTSQLEGGPAENEEDGETVKTYQASAASIAPGYKPSTPVPFLGEA-----EH 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESTEEKIELLITEVPLALEEESPSEGCPSS--EIPMEKEPGEGRISVVDYSYLEGDLPIS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QATEEK----GTE-NKADPSNSPSSGSHSRAWEYYSREKPKQ------EGEAKVE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G---QDLPTPDQDNGYHSLEEBHSLLR------MDPKHCRDNPTQFVPAAGDIPGNTQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARPA----CSNKLID-----444
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                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Mismatches 225;
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ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | :|
----AKTVTGADQIE-----
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERENCE/DOCKET NUMBER: 51523
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YNPONFT------
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315 TGATPHTSAFLKAWVYRPGEDTEEE-----DSDSDSAEEDTAQTGATPHT-SAFLKAWV 367
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                                                                                                                        -----NSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLL 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YSALRALKGREKPA-APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AELIPAS-WQGCP---PLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---YPTSHWEGGPAEDEEDTETVKKAH------OASAASIAP-----GY---- 198
                                                                                                                                                                         --PEHSSGEEDDWES-----SADEAESLKLWNSFC
                                                                                                                                                                                                                                                                                                                                     GS----GESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYIS-----GDEDRKGPWE
                                                                                              -----ATIQTAARI---VPEEPSDSEKDLSGKSDL----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 GADK-----KVGEVVAREEGVSELA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWL--DFAGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 4; Length 578; 5.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
A TITLE OF INVENTION: Progression Elevated Gene-3 and Uses;
TITLE OF INVENTION: Progression Elevated Gene-3 and Uses;
TITLE OF INVENTION: Thereof;
TITLE REPERENCE: A3460B-B;
CURRENT APPLICATION NUMBER: US/09/052,753B
CURRENT APPLICATION NUMBER: PCT/US98/05793
PRIOR APPLICATION NUMBER: PCT/US98/05793
PRIOR APPLICATION NUMBER: 08/812,818
PRIOR APPLICATION NUMBER: 08/812,818
PRIOR PRILING DATE: 1999-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FREESEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTPPPVSENHLPLRETEGNGTPEWSKAAQRLCLDVEAQSSPPKT--
                                                                                                                                                                                                                                                                                                                                                                                                                                       664 EFARDGCRFOKRIQETEDAIGYCLTFEHRERMFNRLQ 700
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11.7%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/09052753B ; Patent No. 6472520
                                                                                                                                                                           522 NSSQSGSLPET------
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                                                                                              YNPONFT-
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Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 LLAPLPGLLOKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 DSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 LOSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HGETEESGSPEQSQAAQRL------CLVEAESSPPETWGLSNVDE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKRLEFLQQANK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 YNA-KPGQDDLREKEMERTAGKATLQPAGLQGAD-------KRLGEVVAREE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G---QDLPTPDQDNGYHSLEEEHSLLR------MDPKHCRDNPTQFVPAAGDIPGNTQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESTEEKIELLTTEVPLALEEESPSEGCPSS--EIPMEKEPGEGRISVVDYSYLEGDLPIS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --YILGGASSDLETSSDPE----- 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | : | : | : AHRAGQGHPCRNAEAEEGGPETTFVCTGNAFLKAWVXRPGEDTEEEDNSDSDSAEEDTAQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AAALLTPTPVSG-NLLP-- 73
                                                                                                                                           485 LPGEKTKGRGEBP--PL-FQVAFYLPGEK------PESPWAAPKLPLRLQRRLRLF
YRPGEDTEEENSDLDSAEEDTAQTGATPHTSAFLKAWVYRPGEDTEEE----NSDLDSAEE
                                                               ----PEHSSGEEDDWES-----SADEAESLKLWNSFC
                                                                                                                -----NSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLL
                                                                                                                                                                                              GS----QESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYIS-----GDEDRKGPWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Paul B. Fisher
TITLE OF INVENTION: Progression Elevated Gene-3 and Uses
TITLE OF INVENTION: Thereof
FILE REPERBNCE: A34608-B
CURRENT APPLICATION NUMBER: US/09/052,753B
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/US98/05793
PRIOR APPLICATION NUMBER: 08/812,818
PRIOR PILING DATE: 1999-03-21
                                                                                                                                                                                                                                                                          EFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 700
                                                                                                                                                                                                                                                                                                21.8%; Pred. Note tive 77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 657
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Sequence 3, Application US/09052753B
Patent No. 6472520
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US-09-052-753B-3
                                      522
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US-08-893-852A-4
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                                                                                                                                                                                                                                                                                                                                                                    418 ----FYLPGQKPAPPWAAPKLPLRLQKRLRSFKAPARNQGPEIPLKGRKVHFSEKVTVH 472
                                                                                                                                                                   280 AFLKAWVYRPGEDTEEE-EDPDLDS-----AEED-----TAHTCTTPH----TS 318
                                                                                                                                                                                                                                      319 AFLKAWVYRPGEDTEEEDDGDWDSAEEDAAQSCTTPHTSAFLKAWVYRPGEDTEEEDDSE 378
                                                                                                                                                                                                                                                                          545 SSAD-EAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHT 603
328 EHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKI------ELLTTEVPLALE 377
                              ------KPSTSVYCPGEAEHRATEEKGTDNKAEPSGSHSRFWBYHTRERPKQEG 246
                                                                EESPSEGCPSSEIP---MEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGAS 434
                                                                                                   ---CS-----GS 279
                                                                                                                                   SDLRTSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTA 494
                                                                                                                                                                                                    495 TIQTAARIVPEEPSDSEKOLSGKSDLENSSQSGSLPET------PEHSSGEEDDWE 544
                                                                                                                                                                                                                                                                                                                                             604 LLSCKVQLLGSQES-----ECPDSVQRDVLS------GGRHTHVKRKKVTFLEEVTEY 650
                                                                                                                                                                                                                                                                                                                                                                                                                651 YIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 700
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08893852A
Patent No. 608058
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Shah, Preeti
APPLICANT: Shah, Purvi
TITLE OP INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,852A
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                   247 ETKPEQHRAGQSHPCQNAESEEGGPETSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF-0341 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF-(TELECOMMUNICATION INFORMATION: TELEPHONE: 415-885-0555 TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 550 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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US-08-893-852A-4
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COUNTRY:
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5.3%; Score 201; DB 3; Length 590;
23.9%; Pred. No. 2e-08;
tive 56; Mismatches 210; Indels 186; Gaps
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TITLE OF INVENTION: IDENTIFICATION OF THE PROGRESSION
TITLE OF INVENTION: BLEVATED GENE-3 AND USES THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,818
FILING DATE:
CLASSIFICATION: 514
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1185 Avenue of the Americas
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                    Best Local Similarity 23.9% Matches 142; Conservative
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STATE: New York
COUNTRY: USA
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FLAVWAGPAQAARRGPWEQLARDRSRFARRIAQAEEKLGPYLTPAFRARAWARL 569
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Similarity 23.9%; Pred. No. 2e-08;
42; Conservative 56; Mismatches 210; Indels 186;
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Patent No. 6472520
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Progression Elevated Gene-3 and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: A34608-B
CURRENT APPLICATION NUMBER: US/09/052,753B
CURRENT FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: PCT/US98/05793
                                                                                                                                                                                                                                                                                                                                                                                    299 KRLEFLOQANKGODLPTPDQDNGYHSLEEHHSLLRMDPKHCRDNP-
        NAME: Chan, Albert Wai-Kit
REGISTRATION NUMBER: 36,479
REFERENCE/DOCKET NUMBER: 51523
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2.
ENGTH: 590 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECTUE TYPE: protein
US-08-821-818-2
ATTORNEY/AGENT INFORMATION:
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Matches 142;
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FLAVWAGPAQAARRGPWEQLARDRSRFARRIAQAEEKIGPYLTPAFRARAWARL 569
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                                                                                                                                                                                                                                                                                                                                      Query Match 5.3%; Score 201; DB 4; Length 590; Best Local Similarity 23.9%; Pred. No. 2e-08; Matches 142; Conservative 56; Mismatches 210; Indels 186;
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Patent No. 6582956
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: NY
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 08/812,818
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 590
TYPE: PRI
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ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                             510 SEKDLSGKSDLENSSQ---SGSLPETPEHSSGEED--DW---ESSADEAESLKLWNSFCN 561
                                                                                                                                                                562 SDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPD 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826 PRRVP-----PDSLPTQGETQPTCLDVIVPE-----DCLHQDISP-----DAVTVPV 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 QLFGGMPPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 PRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKVLIWS
                                                                                                            1201 EHGEEPGRDVLEPTQQELTAAAVPVLAKTEVGQEGEVDWLDGEKVKEEQE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1503;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                             622 SVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEE 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.1%; Score 156.5; DB 3;
Best Local Similarity 20.4%; Pred. No. 0.00061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 147; Conservative 82; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08976255
Patent No. 6136581
GENERAL INFORMATION:
APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.C. COUNTRY: U.C. COMPUTER READABLE FORM:
MEDIUM TYPE: Blorage
TYPE: Storage
American TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE FOOKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1503 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
                  1162 SQDSKATAAVRQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1044 TGSKALEKVEEVEEDSEVLASEKEKDVMPKGPVQEAGAEHLAQGSETGQATPESLEVPEV 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 EGDLPISARPACS----NKLIDYILGGASSDLETSSDPEG-----EDWDEEAEDDGFD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 VVGFQTLTPESSCLREDHCHPQ-PLSAELIPASWQGCPPLSTEGLPEIHHLRMKRLEFLQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 PVLTQTL-PEGKDAHDDMVTSEVDFTSEAVTAT-ETSEALRTEEVTEAGAE-ETTDMVS 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 QANKGQDLP-----TPDQ--DNGYHSLEEE----HSLLRMDPKHCRDN----PTQFVPA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 AGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 605 Q-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTR---WLDFAGVYSALRALKGREKPAAPTAQKSLS----SLQLDSSDPSVTS--PLDW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 LEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPSGPLNIQRIDNFSVVSYL--LNPSYLDCF------PRLEVSYQNSDGNSE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GGSRKRL------GPR----GPR-------AGFRFWPPFFPRRSQAGSSKFPT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 PLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKV-----LIWSQLFGGMF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.4%; Score 167; DB 4; Length 1596;
Best Local Similarity 19.8%; Pred. No. 8.4e-05;
Matches 151; Conservative 112; Mismatches 286; Indels 214; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 SDSSLSDSDLEQDPEGLHLWNSPCSVDPYNPQNFTATIQTAARIVPEEPS-
                                                                                                                                                                                                                                                                                                                                          - 165/34008
                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,277A
FILING DATE:
                                                                                                                                                        CLASSIPTICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/665,401
FILING DATE: 18-JUN-1996
ATTORNEY AGENT INFORMATION:
NAME: Clark, Richard S
REGISTRATION NUMBER: 26,154
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: A30558
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2558
COMPUTER: IBM CC.... DOS
COMPATING SYSTEM: DOS
COMPARE: FREESEQ Version 1.5
COMPARE: FREESEQ VERSION 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERLSTICS:
LENGTH: 1596 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ropology: linear
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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                                                                                                                                          -----PKLKEPDIEGKY-LGKLGVSGMLDLSEDGMDADEED-ENSDD 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                            393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448
                                                                                                                                                                                                             248 -----VGFQTLTPESSCLREDHCHPQPL-SAELIPAS-----WQGCPP----LSTE 288
                                                                                                                                                                                                                                                                                                                      GLPEIHHLRMKRLEFLQQANKGQDLPTPD------QDNGYHSLEEEHSLLRMDPKH 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAESLKLWNSFCNSDDPYNPLNFKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCK 608
GIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPS
                                                 911 RVSVGSSLPELGQELHNKPFSEDHHSHR-RLEKNLEAVETLNQ------LNSKDAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 VQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARD
                                                                                                                                                                                                                                                                                                                                                                                                                            339 CRDNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPL---ALEEESPS--EGCPSSEIPME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 KEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDPEGEDW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DEEAEDD------GFDSDSSLS-----DSDLEQDPEGLHLWNSFCSVDPYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PONFTATIOTAARIVPEEPSDSEKDLSGKSDLENSSOSGSLPETPEHSSGEEDDWESSAD
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APPLICANT: DE SNET, Charles;
TITLE OF INVENTION: REJECTION AUTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       | |: :| | : :| | |: :| | |-----
                                                                                                         GPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEV
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IBM PS/2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08993118
Patent No. 5997872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 -SLLKPTAANAPOPLPED
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 LDWLEEGIHWQYSP------PDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISILQSSPESAQSAFEGFPQSPLQIPVSSSPSYTLLSLFQSSPERTQSTFEGFPQSPLQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSYQNSDGNSEVVGFQTLTPE-----SCLREDHCHPQ-----PLSAELIPA-- 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDP-EG-----LHL-----WNSF 481
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAYE Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
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STRANDEDNESS: single-stranded
TOPOLOGY: linear
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Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
ISOLATED NUCLEIC ACID MOLECULE CODING
FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
AND USES THEREOF
                                                                           590 LSPHY--FPQSPPQGEDSMSPLYPPQSPLQGE---EFQSSLQSPVSICSSSTPSSLPQSF 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        592
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                                                                                                                                                                                                                                                                                 435 SDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDP-EG-----LHL-----WNSF
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                             LEEEHSLLRMDPKHCRD--NPTOF--VPAAGDIPGNTQESTEEKIELLTTEVPLALEE--
                                                                                                                                                       ----ESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 ESIVAISECHTLLSCKVQLLGSQESECPDS-VQRDVLSGGRHTHVKRKKVTFLEE---V
                                                                                                                                                                                                                     -SÖTIGSÖSHW-----
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,528
FILING DATE: APril 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: 11D 5455.2 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fulbright & Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,281B
FILING DATE: April 24, 1998
CLASSIFICATION:
                                                                                                                                                                                                               645 PESSOSPPEGPVQSPLHSPQSPPEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09066281B Patent No. 6475783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: amino acids
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
US-09-066-281B-7
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TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LUCAS, SOPA, TITLE OF INVENTION: 1SO TITLE OF INVENTION: FOR TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York City STATE: New York
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                                                                                  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 LDWLEEGIHWQYSP------PDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 LLSILQSSPESAQSAFEGFPQSPLQIPVSSSFSYTLLSLFQSSPERTQSTFEGFPQSPLQ 479
                                                                                                                         Sequence 7, Application US/08845528C
| Sequence 7, Application US/08845528C
| Patent No. 6027924
| GENERAL INFORMATION:
| APPLICANT: LUCAS, Sophie;
| APPLICANT: BOON-FALLEUR, Thierry
| TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR WAGE-C1 AND USES TITLE OF INVENTION: THEREOF |
| NUMBER OF SEQUENCES: 14 |
| CORRESPONDENCE ADDRESS: | ADDRESSE: Pelfe & Lynch |
| STREET: 805 Third Avenue |
| CITY: New York City |
| STATE: New York City |
| CONTINUED OF SEQUENCES |
| STATE: New York City |
| CONTINUED OF SEQUENCES |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 KVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSP 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 VSYQNSDGNSEVVGFQTLTPE-----SSCLREDHCHPQ-----PLSAELIPA-- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 IPVSSSSSSSTLLSLFQSSPECTQSTFEGFPQSPLQIPQSPPEGENTHSPL--QIVPSLP 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538 EWEDSLSPHYFPQSPPQGEDSLSP-HY-----PPQSPPQGEDSLSPHYFPQSPQGEDS 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 PRRSQA---GSSKFPTPLGPENSGNPTLLS--SAQPETRVSYWTKLLSQLL-APLPGLLQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%; Score 148; DB 3; Length 1142;
20.7%; Pred. No. 0.0021;
tive 90; Mismatches 257; Indels 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acide
STRANDEDNESS: single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 20.7
151, Conservative
876 DEYTSSSD 883
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OPERATING SYSTEM:
SOFTWARE: Wordper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-845-528C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10022
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LOSRLYSNRELGSS-----PSGPLNIQRIDNFSVVSYLL-----NPSYLDCFPR--LE 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDWLEEGIHWQYSP-----PDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEBEHSLLRMDPKHCRD--NPIQF--VPAAGDIPGNIQESTEEKIELLITTEVPLALEE-- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSPHY--FPQSPPQGEDSMSPLYFPQSPLQGE---RFQSSLQSSVSICSSSTPSSLPQSF 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWQG-----CPPLSTEGLPEIHHLRMKRLEFLQQANKGQDLPT----PDQDNGYHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.9%; Score 148; DB 4; Length 1142;
Best Local Similarity 20.7%; Pred. No. 0.0021;
Matches 151; Conservative 90; Mismatches 257; Indels 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645 PESSQSPPEGPVQSPLHSPQSPPEG------MHSQSPLQS-----
                                             storage
                                                                                                                                                                                                                                                                                                                                                                                                     JEL/MAS
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
CLASSIFICATION:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/945,528
FILING DATE: April 5, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
STRANDEDNESS: single-stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         NAME: Mary Anne Schofield
REGISTATION NUMBER: 36,669
REPERENCE/DOCKET NUMBER: LUD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 662-0200
TELEFAX: (202) 662-4643
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PESAPEGED--
                                                             IBM PS/2
                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , TOPOLOGY:
US-09-468-433C-7
                                                                                                         SOFTWARE:
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TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C
TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
NUMBER OF SEQUENCES: 26
                                             41;
                                                                                                               | | :| : | : : | : | | PERTOSTFEGFPOSILOIPMISSFS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSSSLSQSSPVSSFPSSTSSSLSKSSPESPLQSPVISFSSSTSLS----PFSEESSSPV 875
                                                                                                                                                                      KVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSP 139
                                                                                                                                                                                                               STLL--SIFQSSPESAQSTFEGF------PQSP-----LQIPGS-PSFSST 384
                                                                                                                                                                                                                                                     LDWLEEGIHWQYSP------PDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSS 189
                                                                                                                                                                                                                                                                                              LLSL-----PQSSPERTHSTFEGFPQSPLQI------PMTSSF-----SST 419
                                                                                                                                                                                                                                                                                                                                        LOSRLYSNRELGSS-----PSGPLNIQRIDNFSVVSYLL-----NPSYLDCFPR--LE 235
                                                                                                                                                                                                                                                                                                                                                                             LLSILOSSPESAQSAFEGFPOSPLOIPVSSSPSYTLLSLFQSSPERTQSTFEGFPOSPLQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                           VSYQNSDGNSEVVGFQTLTPE-----SCLREDHCHPQ-----PLSAELIPA-- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | : | : | : | : | 480 IPVSSSSSSTLLSLPQSSPECTQSTFEGFPQSPLQIPQSPPEGENTHSPL--QIVPSLP 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEEEHSLLRMDPKHCRD--NPTQF--VPAAGDIPGNTQESTEEKIELLTTEVPLALEE-- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPHY--FPQSPPQGEDSMSPLYFPQSPLQGE---BFQSSLQSPVSICSSSTPSSLPQSF 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGAS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SLSPLQIPQSPLEGEDSLSSLHFPQSPPEWE-- 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DSLSPLHFPQ------PPPQGEDFQSSLQSPVSICSSSTSLSLSPQSFPSSPQSPP 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DWESSADEAESLKLWNSF-----CNSDDPYNPLN--FKAPFQTSGENEKGCRDSKTPS 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGPAQSPLQRPVSSFFSYTLASLLQSSHESPQSPPEGPAQSPLQSP-----VSSFPS 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESIVAISECHTLLSCKVQLLGSQESECPDS-VQRDVLSGGRHTHVKRKKVTFLEE----V 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDP-EG-----LHL-----WNSF 481
                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EWEDSLSPHYFPQSPPQGEDSLSP-HY-----PPQSPPQGEDSLSPHYFPQSPQGEDS
                                                                                     PRRSQA---GSSKFPTFLGPENSGNPTLLS--SAQPETRVSYWTKLLSQLL-APLPGLLQ
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                                           230;
    Length 1142;
  3.9%; Score 148; DB 4; Length 11.
20.7%; Pred. No. 0.0021;
ive 90; Mismatches 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jaworski L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fulbright & Jaworski L.L. STREET: 801 Pennsylvania Avenue, NW CITY: Washington STATE: District of Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09468433C Patent No. 6680191
GENERAL INFORMATION:
                     al Similarity 20.7
151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PESAPEGED-
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	FILING DATE: 14-APR-1998 CLASSIFICATION:		
	ALIONELI MAKI, David J. REGISTRATION NUMBER: 31,392		
; INFC	TELEFAX: (2 (206) 682-6031 TELEFAX: SEQ ID NO: 4:		
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; ; W(; US-09-(; TOPOLOGY: linear ; MOLECULE TYPE: protein US-09-060-410-4		
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seq length: 200000000
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Post-processing:

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Sequence:

protein

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Scoring table:

Sequence 529, App Sequence 302963, Sequence 42484, A Sequence 276711, Sequence 276711, Sequence 5, Appl Sequence 195, App Sequence 195, App Sequence 1, Appli Sequence 4, Appli Sequence 3249, A Sequence 7, Appli Sequence 7, Appli Sequence 165014, Sequence 165014, Sequence 363, Appli Sequence 363, Appli Sequence 363, Appli Sequence 2, Appli

Sequence 2, Appli Sequence 36776, A Sequence 13, Appli Sequence 18, Appl Sequence 18, Appl Sequence 124762, Sequence 2174, App Sequence 2174, App Sequence 2174, Appl Sequence 2174, Appl Sequence 2174, Appli Sequence 52462, Appl Sequence 16, Appli Sequence 17, Appli Sequence 27, Appli Sequence 240, Appli

1, Appli 67803, A 138582,

Sequence Sequence Sequence

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3804 3627 3627 2223 8133 259.5 236 236 219 219 201

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Result Š

Db 361 TEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVUDYSYLEGDLPISARPA 420	RESULT 2 US-09-925-299-941 Sequence 941, Application US/09925299 Sequence 941, Application US/09925299 Patent No. US20020055627A1 GENERAL INFORMATION: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102 CURRENT APPLICATION NUMBER: US/09/925,299 CURRENT APPLICATION NUMBER: PCT/US00/05883 PRIOR FILING DATE: 2000-03-08 PRIOR FILING DATE: 1999-03-12 PRIOR PILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556 SOFTWARE PATENTIN Ver. 2.0 SEQ ID NO 811 LENGTH: 707 TYRE: PRI TYR		Query Match 95.3%; Score 3627; DB 9; Length 707; Best Local Similarity 98.8%; Pred. No. 3e-265; Indels 0; Gaps 0; Matches 683; Conservative 1; Mismatches 7; Indels 0; Gaps 0; QY 23 PFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRYSYWTKLLSQLLAPLPGLLQKVL 82	OY 83 IWSOLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAOKSLSSLOLDSSDPSVTSPLDW 142
85 134.5 3.5 1253 14 US-10-363-798-2 Sequence 2, Appli 86 134.5 3.5 1692 17 US-10-732-923-8431 Sequence 9431, Appl 87 134.5 3.5 1969 9 US-09-839-479-71 Sequence 71, Appl 89 134.5 3.5 1969 15 US-10-376-573-72 Sequence 72, Appl 90 134.5 3.5 1969 15 US-10-702-148-71 Sequence 71, Appl 90 134.5 3.5 2468 16 US-10-755-889-615 Sequence 216, Appl 91 134.5 3.5 2519 18 US-10-489-740-216 Sequence 216, Appl 92 134.5 3.5 252 18 US-10-450-763-86995 Sequence 8127, Appl 93 134.5 3.5 3579 17 US-10-732-923-8327 Sequence 8327, Appl 96 134.5 3.5 3579 17 US-10-732-923-8329 Sequence 8326, Appl 97 134.5 3.5 3579 17 US-10-732-923-8329 Sequence 8326, Appl 97 134.5 3.5 3579 17 US-10-732-923-8329 Sequence 8329, Appl 97 134.5 3.5 1439 16 US-10-437-993-803 Sequence 803, Appl 97 134.5 3.5 1439 16 US-10-437-993-803 Sequence 264340, Appl 97 133.5 3.5 446 16 US-10-437-993-803 Sequence 264340, Appl 97 133.5 3.5 446 16 US-10-437-993-803 Sequence 264340, Appl 97 133.5 3.5 446 16 US-10-425-115-264340	JEGURES 2, Application US/10650482 Publication No. US20040142345a1 Fublication No. US20040142345a1 GENERAL INFORMATION: APPLICANT: Ron, David APPLICANT: Ron, David APPLICANT: Solusse, Celine TITLE OF INVENTION: PHCSPHATASE SUBUNIT TITLE OF INVENTION: PHCSPHATASE SUBUNIT TITLE OF INVENTION: WHORER: US/10/650,482 CURRENT APPLICATION NUMBER: US/10/650,482 CURRENT PILING DATE: 2002-09-06 PRIOR FILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version 3.1 SEQ ID NO 2 LENGRANT RILL SEQ ID NO 2 LENGRANTSM: Homo sapiens US2-10-650-482-2	Query Match 100.0%; Score 3804; DB 16; Length 713; Best Local Similarity 100.0%; Pred. No. 1.2e-278; Adding 100.0%; Adding 100.0%;	OY 121 QKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQL 180	OY 241 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQCCPPLSTEGLPEIHHLRMKR 300 241 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQCCPPLSTEGLPEIHHLRMKR 300 241 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQCCPPLSTEGLPEIHHLRMKR 300 QY 301 LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES 360

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (271)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                            HSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPS 376
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US-09-925-299-941
SPSGLLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLRE 256
                        VQRDVLSGGRHTHVKRKKVTFLERVTEYY1SGDEDRKGPWEEFARDGCRFQKRIQETEDA
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Publication No. US2003004061749
GENERAL INFORMATION:
FILLE APPLICATT Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Ant.
FILLE REFERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05883
PRIOR APPLICATION NUMBER: 607/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEG ID NOS: 1556
SOFTWARE PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                             IGYCLTFEHRERMFNRLQGTCFKGLNVLKQC 713
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LOCATION: (307)
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23 PFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQXVL

Matches 683; Conservative

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; Sequence 4, Application US/10650482
; Publication No. US20040142345A1
; GENERAL INFORMATION:
APPLICANT: Ron, David
; APPLICANT: Ron, David
; TITLE OF INVENTION: METHODS OF SCREENING TEST COMPOUNDS USING GADD34L, AN eIF21;
; TITLE OF INVENTION: PHOSPHATAES SUBUNIT
; FILE REFERENCE: 5986/11/12-US1
; CURRENT PELING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/408,679
; PRIOR PILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID 0.4
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17 PSVSRRSQAGSSKRPTPLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKVL 76
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ORGANISM: Mus musculus
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US-10-650-482-4
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343 VYWPGEDTEEE-EDEEEDEDSDSGSDEEGGEAEASSSTPATGVFLKSW------VYQPG 394
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                                                                                                               GYCLTFEHRERMFNRLOGTCFKGLNVLKOC 713
                                                                                                                              GYCLTFEHRERMFNRLQGTCFKGLNVLKQC 153
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US-10-755-889-90
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APPLICANT: Hyear Inc.
TILLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TILLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
FILLE REPRENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
FILLE OF INTOR APPLICATION NUMBER: US09/488,725
FRIOR FILLING DATE: 2000-01-21
FRIOR PELICATION NUMBER: US09/552,317
FRIOR APPLICATION NUMBER: US09/552,317
FRIOR APPLICATION NUMBER: US09/552,317
                                                                                                                    QKSLSSLQLD-SSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQ
                                                                                                                                                                       SAGGGOFVGFRILIPESCYLSEDGCHPQPLRAEMSATAWRRCPPLSTEGLPEIHHRRWR
                                                                                                                                                                                                                                                                           295 WLVFL-QPNQQQDLPTLDQDNGYHSLEEEHNLLRMDPQHCTDNPAQAVSPAADRP---E
                                                                                                                                                                                                                                                                                                                               350 PTEKKPELVIQEV----SQSPQGSSLFCELPVEKECEEDHTNATDLSDRGESLPVSTRP
                                                                                                                                                                                                                                                                                                                                                                                 405 VCSNKLIDYILGGAPSDLEASSDSESEDWGEEPEDDGFDSDGSLSESDVEQDSEGLHLWN
                                                                                                                                                                                                                                                                                                                                                                                                                                    SFHSVDPYKPQNFTATIQTAARIAPRDPSDSGTSWSGSCGV-GSCQEGPLPETPDHSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BDDWEPSADEAENLKUMNSFCHSEDPYNLINFKAPFQPSGKNWKGRQDSKASSEVTVAFS
MEPGTGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV
                                                  SYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTA
                                                                                                                                                                                                                                                             RLEFLOQANKGODLPTPDQDNGYHSLBEBHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQE
                                                                                                                                                                                                                                                                                                                STEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARP
                                                                                                                                                                                                                                                                                                                                                                    ACSINKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 963, Application US/10296115
Publication No. US20040053248A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 150; Conservative
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SEQ ID NO 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-296-115-963
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Sequence 90, Application US/10755899;
Sequence 90, Application US/10755899;
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Hyers Squibb Company
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: DO284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR PILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.2
SEQ ID NO 90
LENGTH 674
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                                                                                                                                                                    QRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPGEEAEDSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TSVSPRSSGSDPRS 259
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                                                        63
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                                        4 DPYNPLNFKAPFOTSGENEKGCRDSKTPSESIVAISECHTLLSCKVOLLGSQESECPDSV
DPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSV
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                                                                                                                           QRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAI
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Db 315 TGATPHTSAFLKAWVYRPGEDTEEEDSDSDSAEEDTAQUGATPHT-SAFLKAWV 367 Qy 487 YNPONFT	" v cmx > a > a > a > a > a > a
03	Query Match 6.2%; Score 236; DB 9; Length 657;

Db 199	545 SSAD-EAESLKLWNSFCNSDDPYNPLNFKAPFOTGENERGCRDSKTPSESIVAISECHT	RESULT 10 RESULT 10 RESULT 10 Sequence 7, Application US/10277603 Fublication No. US20030219376A1 SEQUENCE 7, Application US/102776A1 Fublicant INFORMATION: PROGRESSION ELEVATED GENE-3 AND USES TITLE OF INVENTION: THEREOF FILE REPERENCE: AJ4608-B-A CURRENT APPLICATION NUMBER: US/10/277,603 CURRENT FILING DATE: 1998-03-31 FRIOR FILING DATE: 1998-03-31 FRIOR FILING DATE: 1998-03-31 FRIOR FILING DATE: 1998-03-32 NUMBER OF EQUID NOS: 8 SOFTWARE: FREEFE SECTION NUMBER: PCT/US98/05793 NUMBER OF EQUID NOS: 8 SEQ ID NO 7 LENGTH: 578 TENGTH: 578	CARGANISM: Human S.8%; Score 219; DB 15; Length 578; Query Match
Qy 417 ARPACSNKLID	425 DIAQTGATPHTSPFLKAWYRPGEDTEEEEDSENVAPGDSETADSSQSPCLQPQRC 5 1 1 1 1 1 1 1 1 1	RESULT 9 US-09-052-753-7 is Sequence 7, Application US/09052753A is Sequence 7, Application US/09052753A is Patent No. US20010014734A1 is GENERAL INFORMATION: is APPLICANT: Fisher: Paul B. is TILE REFERENCE: 0575/51523-B/JPW/JSG is CURRENT APPLICATION UNMBER: US/09/052,753A is CURRENT PILING DATE: 1998-03-31 is NUMBER OF SEQ ID NOS: 8 is SEQ ID NO 7 is LENGTH: 578 is TYPE: PATENTIN Ver. 2.1 is COTWARE: PATENTIN Ver. 2.1	Query Match 5.8%; Score 219; DB 9; Length 578; Best Local Similarity 21.7%; Pred. No. 1.6e-07; Matches 155; Conservative 79; Mismatches 223; Indels 258; Gaps 34; Qy 53 SAQPETRYSYWTKLLS-QLLAPLPGLLQKVLIMSQLFGGMFPTRML-DFAGV 102 bb 4 SPRPE-HVLHWKEAHSFYLLSPLMGFLSRA-NFRELGEPEVSEAMLAETVAGANGIQADA 60 Qy 103YSALRALKGREKDA-APTAGASLQLDSSDPSVTSPLDWLEEGIHWQY 151 bb 61 LLTPPPVSENHLPILETGGNGTPEWSKAAQRLCLDVEAQSSPFXT

Qy 485 DPYNPQNFTATIQTAARIVPEEPSDSEKOLSGKSDLE 521 Db 283 WVYRPGEDTEDDDDSDWGSAEEGGKALSSPTSPEHDFLKAWYRPGEDTEDDDDSDWG 340 Qy 522 NSSQSGSLPETPEHSSGEEDDWESSADEAES	277.603-2 ence 2, Application ication No. US20030 RAL INFORMATION: LICANT: Fisher, Pau LE OF INVENTION: PR LE OF INVENTION: PR LE REFERENCE: A34608 RENT APPLICATION NUMB OR RILING DATE: OR APPLICATION NUMB OR FILING DATE:	NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 590 TYPE: PRT ORGANISM: Rat ORGANISM: Rat S-10-277-603-2 Query Match Best Local Similarity 23.9%; Pred. No. 3.8e-06; Matches 142; Conservative 56; Mismatches 210; Indels 186; Gaps	Oy 245 SEVUCEQTITPESSCIREDHCHPQPLSAELIPASWQGCPLSTEGLPEIHHLRM 298
Db 164YPTSHWEGGFAEDEEDTETVKKAHQASAASIAPGY 198 328 EHSILIRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKIELLITTEVPLALE 377 Db 199		APPLICANT: Fisher, Paul B. TITLE OF INVENTION: PROGRESSION ELEVATED GENE-3 AND USES THEREOF FILE REPRENCE: 0575/51523-B/DW/JSG CURRENT PRILING DATE: 1998-03-31 CURRENT FILING DATE: 1998-03-31 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 2 LENGTH: 590 TYPE: PRT OCKANISM: Rat US-052-753-2	Query Match S.3%; Score 201; DB 9; Length 590; Best Local Similarity 23.9%; Pred. No. 3.88-06; Matches 142; Conservative 56; Mismatches 210; Indels 186; Gaps 29; QY 245 SEVGFQTLTPESSCLREDHCHOPLSAEL

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Sequence 13, Application US/10097534

Publication No. US20030049607A1

GENURAL INFORMATION:
APPLICANT: GREENER TSVIKA
APPLICANT: GREENER TSVIKA
APPLICANT: GREENER TSVIKA
APPLICANT: REISS, YUVAL
APPLICANT: ROMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/275,224
PRIOR PEPLICATION NUMBER: 60/275,224
PRIOR PEPLICATION NUMBER: 60/275,224
PRIOR PEPLICATION NUMBER: 60/310,170
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
SEQ ID NOS: 71
SEQ ID NO 13
                                                                                                                                                                                                                                                               -----QVTEERAATAQKEEPSTLPNNVPAQE 1200
                                                                                                                                         |: | : | : | : | : | 104 TADVDHVA--TCQVIKLQQLMEQAVAPESSETLTDSETNGSTPLADSDTADGTQQDETID 1161
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                                                                                                                                                                                                                                                                                                                  510 SEKDLSGKSDLENSSQ---SGSLPETPEHSSGEED--DW---ESSADEAESLKLWNSFCN 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 DWLEEGIHWQYSPPD-LKLELKAKGSALDPAAQAF-----LLEQQLWGVELLPSS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOSRLYSNRELG-------SSPSGPLNIQRIDNFSVVSYLLNPSYLDC 230
                                                                                                                                                                                                                                                                                                                                                                                                                     562 SDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPD 621
                                                                                                                                                                                                              SDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAARIVPEEPS-----D
                                                                                                           EGDLPISARPACS----NKLIDYILGGASSDLETSSDPEG------EDWDEEAEDDGFD
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                                                                                                                                                                                                                                                                                                                                               622 SVQRDVLSGGRHTHVKRKKKVTFLEEVTEYYISGDEDRKGPWEE 664
                                                                                                                                                                                                                                                                 1162 SQDSKATAAVRQS------
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TYPE: PRT
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                                                                                                                                                                                                                    SAEBEGKALSSPTSPEHDFLKAWVXRPGEDTEDDQDSDWGSAEKDGLAQTFATPHTSAFL 400
                                                                                   KLWNSFCNSDDPYN-----PLNFKA--PFQTSGENEKGCRDSKTPSESIVAISEC-HT 603
                                                                                                                                KTW-VCCPGEDTEDDDCEVVVPEDSEAADPDKSPSHEAQGC----LPGEQTEGLVEAEHS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           673 GSSKKRARKASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQDQAQGSSSPE 732
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                                                                                                                                                                                      LLSCKVQLLGSQES-----ECPDSVQRDVL-----SGGRHTHVKRKKVTFLEEVTEY
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PLAVWAGPAQAARRGPWEQLARDRSRFARRIAQAEEKLGPYLTPAFRARAWARL 569
                                                                                                                                                                                                                                                                                          651 YIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRL
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4.4%; Score 167; DB 9; Length 1596;
Best Local Similarity 19.8%; Pred. No. 0.0061;
Matches 151; Conservative 112; Mismatches 286; Indels 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Trwin H. Gelman
APPLICANT: Susan G. Jaken
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: A0558-A-FWC-A 070156.0597
CURRENT APPLICATION NUMBER: US/09/902,432
CURRENT APPLICATION NUMBER: US/09/902,432
FRIOR APPLICATION NUMBER: 08/978,277
PRIOR PILING DATE: 1997-11-25
PRIOR FILING DATE: 1996-06-18
SUPPRIOR FILING DATE: 1996-04-19
SEQ ID NO SEQ ID NOS: 35
SOUTHARE: PASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09902432
Patent No. US20020160002Al
GENERAL INFORMATION:
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US-09-902-432-4
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NAME/KEY: DOMAIN
LOCATION: (1257)..(1562)
COTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: PFam, accession name HECT, E-value=4.3e-127, PFam score of 435.6
US-10-450-763-57852
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OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: eMAIRX, accession number PF00632C, p-value=3.302e-23, raw score
OTHER INFORMATION: 20.66
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PPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGL 290
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                                                        - PRSEAPESSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGMVSVGPEGA 394
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; Publication No. US20050196754A1
; REBELL INFORMATION:
; APPLICAMT: HYBOR, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFREENCE: 796CTP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT PILING DATE: 2003-06-11
; PRIOR PILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; RIOR FILING DATE: 2000-03-31
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US-10-450-763-57852
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                                                                                                   31 AGSSKFPTP-LGPENSGNPTLLSSAQPETRVSYWT-KLLSQLLAPLPGL-LQKVLIWSQL
                                                                                                                                                                   123 SGALRATTPSVTVKNSAAPIPKSIGADETVQGQGSRRLISFSLSDFQAMGLKK----
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20.9%; Pred. No. 0.018;
iive 99; Mismatches 277; Indels
                               161; Conservative
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Result
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1 MEPGTGGSRKRLGPRAGFRF.....RMFNRLQGTCFKGLNVLKQC 713
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Database

Sequence 2, Appli Sequence 1955, A Sequence 18965, A Sequence 2348, Ap Sequence 241, App Sequence 941, App Sequence 963, App Sequence 963, App Sequence 15743, A Sequence 15743, A Sequence 15743, A Sequence 1956, Ap Sequence 1451, A Sequence 22543, A Sequence 2, Appli Sequence 14318, A Sequence 2541, A Sequence 1816, Ap Sequence 1818, Appli Sequence 1818, Appli

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 2337, Ap Sequence 2337, Ap Sequence 2337, Ap Sequence 5909, Ap Sequence 5909, Ap

Sequence 38864, 7 Sequence 23675, Sequence 12944, A

SUMMARIES

OY 181 WGVELLPSSLOSRLYSDRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN 240 181 WGVELLPSSLOSRLYSDRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN 240 241 SDGNSEVVGFOTLTPESSCLREDHCHPOPLSAELIPASWGCCPLSTEGLPEIHHLRMKR 300 241 SDGNSEVVGFOTLTPESSCLREDHCHPOPLSAELIPASWGCCPLSTEGLPEIHHLRMKR 300 242 SDGNSEVVGFOTLTPESSCLREDHCHPOPLSAELIPASWGCPPLSTEGLPEIHHLRMKR 300 OY 301 LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRNDPKHCRDNPTOPVPAAGDIPGNTQES 360 DD 301 LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRNDPKHCRDNPTOFVPAAGDIPGNTQES 360 OY 301 LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRNDPKHCRDNPTQFVPAAGDIPGNTQES 360 OY 421 CSNKLIDYILGGASSDLETSSDPGGDNDERAEDGERGRISVVDYSYLEGDLPISARPA 420 ON 421 CSNKLIDYILGGASSDLETSSDPGGDNDEBAEDDGPDSSSLSDSLEODPRGLHLWNS 480 OY 421 CSNKLIDYILGGASSDLETSSDPGGDNDEBAEDDGPDSSSLSDSDLEODPRGLHLWNS 480 OY 421 CSNKLIDYILGGASSDLETSSDPGGDNDEBAEDGFDSSSLSDSDLEODPRGLHLWNS 480 OY 421 CSNKLIDYILGGASSDLETSSDPGGDNDEBAEDGFDSSSLSDSDLEODPRGLHLWNS 480 OY 421 CSNKLIDYILGGASSDLETSSDPGGDNDEBAEDGFDSSSLSDSDLEOPPRGSEE 540 DD 541 DDWESSADEASSLKLWNSFCNSDDPYNPLNFKAPPQTSGRSKTPSSESIVAISE 600 OY 601 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGKSDLENSSGSSLPETPEHSSGEE 540 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGKSULENYTREEVTFYYISGDEDRKG 660 OHLILLSCKVQLLGSQESECPDSVQRDVLSGGKHTHVRRKKVTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKVTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKVTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVGRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVGRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVGRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDEDRKG 660 CHTLLSCKVQLLGSQESECPDSVGRDVLSGGRHTHVRRKKYTFLEEVTFYYISGDED	RESULT 2 US-10-205E US-10-170-205E	
Sequence 29941, A Sequence 29941, A Sequence 24058, A Sequence 30390, A Sequence 31983, A Sequence 31983, A Sequence 24710, A Sequence 25036, A Sequence 7969, Ap Sequence 769, Ap Sequence 62, Appl Sequence 1795, Ap Sequence 2188, Ap Sequence 241, App Sequence 241, App Sequence 241, App	TEST COMPOUNDS USING GADD34L, AN elF2alpha-4; DB 32; Length 713; 2.5e-297; AGSSKPPTPLGPENSGNPTLLSSAQPETRV 60	18
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77 77 77 77 77 77 77 77 77 77 77 77 77	RESULT 1 US-10-650-482-2 Sequence 2, Application US/1065048 Sequence 2, Application US/1065048 Sequence 2, Application US/1065048 Sequence 2, Application US/1065048 SEQUENCENT: Jourse, Celine TITLE OF INVENTION: PHOSPHATASE FILE REPRENENCE: 5986/L1712-US1 CURRENT APPLICATION NUMBER: US/10 CURRENT PILING DATE: 2002-09-06 NUMBER OF SEQ ID NOS: 10 SOFTWARE: PATTION NUMBER: US/10 SEQ ID NO 2 LENGTH: 713 TYPE: PRT CORGANISM: Homo sapiens US-10-650-482-2 Query Match Matches 713; Conservative 0; Matches 714	oy ga

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                                                                                                                              LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001460.7
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116313
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 17655
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                                                     241 SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRWKR 300  
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181 WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN 240
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US-60-452-680-17655
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GENERAL INFORMATION:
APPLICANT: OTA, TOSHIO
APPLICANT: SAFIC, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SUBJURANA, TOWOYASU
APPLICANT: SUBJURANA, TOWOYASU
APPLICANT: SUBJURANA, TOWOYASU
APPLICANT: NACAMATSU, AI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/10/917,503
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                     Length 713;
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                   Score 3794; DB 20;
Pred. No. 1.6e-296;
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                                             2; Mismatches
                     Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
US-09-629-469A-18965
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Pred. No. 1.6e-296;
2; Mismatches 0;
CURRENT FILLING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US/09/629,469
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 1000-07-29
PRIOR PAPLICATION NUMBER: UP 1999-248036
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-07-29
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1900-02-17
NUMBER OF SEG ID NOS: 19025
SOCTUMER: PARENT VAF. 2.1
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Best Local Similarity 99.7%;
Matches 711; Conservative 2
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US-10-917-503-18965
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              Length 720;
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                                                                                                                                                        APPLICATION: Nucleic Acids, Proteins, and Ant.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant.
FILLE REFERENCE: PMOUDICIAN
CURRENT APPLICATION NUMBER: 08/10/222,911
CURRENT FILING DATE: 2002-08-19
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3789; DB 28;
Pred. No. 4.2e-296;
1; Mismatches 1;
                                                                                                              US-10-222-911-2348
; Sequence 2348, Application US/10222911
; GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 711; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo
US-10-222-911-2348
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                                                                                                     Sequence 2346, Application US/09757028
GENERAL INFORMATION:
FAPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PW001
CURRENT FILING DATE: 2001-09
FRIOR PILING DATE: 2001-01-09
FRIOR APPLICATION NUMBER: 60/179,065
FRIOR PLILNG DATE: 2000-01-31
FRIOR PLILNG DATE: 2000-02-34
FRIOR FLING DATE: 2000-02-04
FRIOR FLING DATE: 200-02-04
FRIOR FLING DATE: 2000-02-04
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99.7%; Pred. No. 4.2e-296;
ive 1; Mismatches 1;
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Best Local Similarity 99.7
Matches 711; Conservative
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; ORGANISM: Homo sapiens
US-09-757-028-2348
                                                                              RESULT 6
US-09-757-028-2348
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
NAME/KEY: SITE
LOCATION: (265)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (271)
                                 496
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                                                                     VPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEEDDWESSADBAESLKLWNSFCNS
                                                                                         VPEEPSDSEKDLSGKSDLENSQSGSLPETPEHSSGEEDDWESSADEAESLKLWNSFCNS
                                                                                                                                            DDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDS
                                                                                                                                                              DDPYNPLNPKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDS
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PEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAARI
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ilarity 98.8%; Pred. No. 5e-283;
Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                    683 IGYCLTFEHRERMFNRLQGTCFKGLNVLKQC 713
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SEQ ID NO 941
                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 941, Application US/09925299; GENERAL INFORMATION:
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Best Local Similarity
Matches 683; Conserv
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                                                                                                                                                       RESULT 8
PCT-US00-05883-941
Scr-US00-05883-941
GENERAL INPORMATION:
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Human Colon Cancer Associated Gene Sequences and Polypeptides
FILE REFERENCE: PA102PCT
CURRENT APPLICATION NUMBER: PCT/US00/05883
CURRENT APPLICATION NUMBER: PCT/US00/05883
CURRENT APPLICATION NUMBER: 60/124,270
SARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 1556
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                    CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYY1SGDEDRKG
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CHILLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKG
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NAMB/KEY: SITE
LOCATION: (307)
CHER INFORMATION: X
PCT-US00-05883-941
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NAME/KEY: SITE
LOCATION: (265)
OTHER INFORMATION: X
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NAME/KEY: SITE
LOCATION: (271)
OTHER INFORMATION: X
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Best Local Similarity
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240 NSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMK 299
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                                                                               295 WLVFL-QPNQGQDLPTLDQDNGYHSLEBEHNLLRWDPQHCTDNPAQAVSPAADRP----E
                                                                                                                                                300 RLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQE
                                                                                                                               360 STEEKIELLTTEVPLALEEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARP
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                                                                                                                                                                                                                                                                                                                         540 EDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAIS
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: PCT/US00/35017A
CURRENT FILING DATE: 2000-12-22
REICH APPLICATION NUMBER: US09/488,725
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NOS: 1478
TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 9.9e-57;
Matches 150; Conservative 0; Mismatches 0;
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' GENERAL INFORMATION:
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PCT-US00-35017A-963
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                                                                                                                                  EGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSD
                                                                                                                                                                                                                                                                VPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEEDDWESSADEAESLKLWNSFCNS
                                                 HSLEBEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPS
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65.0%; Pred. No. 1.4e-169;
tive 53; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 IGYCLIFEHRERMFNRLQGICFKGLNVLKQC 707
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Seguence 4. Application US/10650482
Sequence 5. Application US/10650482
APPLICANT: Bon, David
TITLE OF INVENTION: METHODS OF SCREENING TES'
TITLE OF INVENTION: PROSPERTASE SUBUNIT
FILE REPRENCE: 5986/11/12-US1
CURRENT APPLICATION NUMBER: US/10/650,482
CURRENT FILING DATE: 2002-08-28
FRIOR FULING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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nes 456; Conservative
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GENERAL INFORMATION:
APPLICANT: BONAZZI, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624 QRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWBEFARDGCRFQKRIQETEDAI 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 ORDVLSGGRHTHVKRKKVTFLEEVTBYYISGDEDRKGPWEEFARDGCKFQKRIQETEDAI 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SQESECPDSVQRDVLSGGRHTHVYRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCSVQ 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 DPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 15743, Application PC/TUS0114827
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
| FILE REFERENCE: 21272-104
| CURRENT APPLICATION NUMBER: PCT/US01/14827
| CURRENT FILING DATE: 2001-05-16
| PRIOR APPLICATION NUMBER: 09/577,408
| NUMBER OF SEQ ID NOS: 16102
| SOFTWARE: CUSTOM
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
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21.4%; Score 813; DB 28;
Best Local Similarity 100.0%; Pred. No. 9.9e-57;
Matches 150; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 GYCLTFEHRERMFNRLQGTCFKGLNVLKQC 153
                                                               CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
LENGTH: 153
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ORGANISM: Homo sapiens
PCT-US01-14827-15743
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CORGANISM: Homo sapiens
US-10-296-115-963
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US-60-177-571-4491
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| Sequence 4519, Application US/60162247
| Sequence 4519, Application US/60162247
| GENERAL INFORMATION:
| APPLICANT: Bonazal, Vivien | TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, TITLE OF INVENTION: USES THEREOF | CURRENT APPLICATION NUMBER: US/60/162,247 | CURRENT FILING DATE: 1999-10-29 | NUMBER OF SEQ ID NOS: 5442 | SEQ ID NO 4518 | SEQ ID NO 4518 | LIGGIN 17318 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 VIFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.6%; Score 402; DB 37; Length 73; Best Local Similarity 100.0%; Pred. No. 4.8e-24; Matches 73; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 399; DB 37; Length 73; ilarity 98.6%; Pred. No. 8.4e-24; Conservative 1; Mismatches 0; Indels
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                                  FILE REFERENCE: CL000201
CURRENT APPLICATION NUMBER: US/60/177,571
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4491
LENGTH: 73
TITLE OF INVENTION: AND USES THEREOF
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Best Local Similarity
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US-60-177-571-4491
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US-60-162-247-4518
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Title: Perfect score:

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Scoring table:

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Sequence 904, App Sequence 1564, Ap Sequence 1264, Ap Sequence 1260, A Sequence 1260, A Sequence 1260, Ap Sequence 1059, Ap Sequence 1036, App Sequence 11961, App Sequence 1
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Sequence 4
Sequence 9
US-10-330-773A-904
US-11-051-720-1563
US-11-051-720-1564
US-11-097-143-9906
US-10-0450-763-32497
US-11-060-763-52460
US-11-0450-763-36776
US-11-097-143-18597
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US-11-097-143-1059
US-11-097-143-1059
US-11-097-143-1036
US-10-560-64-965
US-10-940-774A-1036
US-10-940-774A-1036
US-10-940-774A-1037
US-11-124-368A-291
US-11-097-143-17961
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US-60-710-726-548
US-10-940-7710-364
US-11-489-448-1881
US-10-489-448-1881
US-10-450-76-4059
US-60-664-936-1044
PCT-US04-37982-299
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US-10-990-328A-12859
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                               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-11-097-144-31983

US-10-97-144-31983

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US-10-865-372-46-2

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                                                                                                                                                            September 16, 2005, 10:42:43
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                                                                                                                 protein search, using sw model
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                                            -----VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIG 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 SPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQ 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------KPSTSVYCPGEAEHRATEEKGTDNKAEPSGSHSRVWEYHTRERPKQEG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YSALRALKGREKPA-APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 AELIPAS-WQGCP---PLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKI------BLLTTEVPLALE 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQ 497
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  196 AEDWGBAEPCPFRVAI-----YVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHD
                                                                                     545 PDPETPLKARKVRFSEKVTVHFLAVWAGPAQAARQGPWEQLARDRSRFARRITQAQEELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|: | :| : | | | | | | | 4 SPRPQ-HVLHWKEAHSFYLLSPLMGFLSRA--WSRLRGPEVSEAWLAETVAGANQIEADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWL--DFAGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: rat/human chimera (artificial) amino acid sequence; OTHER INFORMATION: of rPEG-3 1-347 + hGADD34 422-674
US-11-040-219-5
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                                                                                                                                                                                                                                            RESULT 2
US-11-040-219-5
; Sequence 5, Application US/11040219
; GENERAL INFORMATION:
; TITLE OF INVENTION: Chimeric tumor suppressor gene and
; TITLE OF INVENTION: Chimeric tumor suppressor gene and
; TITLE OF INVENTION: Proctein
; TITLE OF INVENTION: NUMBER: US/11/040,219
; CURRENT FILING DATE: 2005-01-21
; NUMBER OF SEQ ID NOS: 12
; SOFFWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 GADK-----KVGEVVAREEGVSKLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDID---EHNGK-----PGODGLREQEVEHTAGLP-TLQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP---
                                                                                                                                    685 YCLTFEHRERMFNRLQGTCFKGLNVLKQ 712
                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPEREAEDSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGOGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 FVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSE-----IPMEKEPG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 -EGEDWDERAEDDGFDSDSSLSDSDLEQDPEG-----LHLWNSFCSVDPYNPONF 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 WPGEDTEEE-EDEEEDEDSDSGSDEEGGEAEASSSTPATGVFLKSW------VYQPGED 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP-------ETPEH-- 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 T------EEEEDEDSDIGSAEDEREAETSASTPPASAFLKAWVYRPGEDTEEEED 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRECCPAVE---EEDD--------EEAVKKEAHRTSTSALSPGSKPSTWVSCP-- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GEEENQATEDKRIERSKGARK-------TSVSPRSSGSDPRS 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 ----SSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNPKAPFQTSG-----ENEKG 584
  App
App
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286,
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Sequence Sequence S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 260.5; DB 7; Length (Best Local Similarity 21.9%; Pred. No. 1.3e-06; Matches 164; Conservative 80; Mismatches 263; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR-
                                                                                                                                                                                                                                                                           gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: human GADD34 amino acid sequence
US-11-040-219-2
                                                                                                                                                                                                 Sequence 2, Application US/11040219;
SERERAL INFORMATION:
APPLICANT: Paul Fisher
ITLE OF INVENTION: Chimeric tumor suppressor gen;
ITLE OF INVENTION: proceedin
FILE REPERENCE: 36351 (070050.2617);
CURRENT APPLICATION NUMBER: US/11/040,219;
CURRENT FILING DATE: 2005-01-21;
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
US-60-671-501-233
PCT-US05-14965-286
                                                                                       ALIGNMENTS
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737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                         RESULT 1
US-11-040-219-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 674
131
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                                                                                                                                     -VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFOKRIOETEDAIGYCLTF 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733 PAGSPSEGE------GVSTW-ESFKRLVTPRKKSKSKLEEKAEDSSVEQLSTEIE 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTR---WLDPAGVYSALRALKGREKPAAPTAQKSLS----SLQLDSSDPSVTS--PLDW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 LEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 SPSGPLNIQRIDNFSVVSYL--LNPSYLDCF------PRLEVSYQNSDGNSE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ::: || |: :: || |: 867 TLVHTVSVAVIDGTRAVTSVEERSPSWISASVTEPLEHTAGEAMPPVEEVTEKDIIAEET 926
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 | :| : :| |: | ----DPHPSHP-DQRAHFRGWGYRPGKETEEEEAAEDWG 431
                                                                                 432 EAEPCPFRVAI------YVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHDPDPET 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 PVLTQTL-PEGKDAHDDMVTSEVDFTSEAVTAT-ETSBALRTEEVTEASGAE-ETTDMVS 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKV-----LIWSQLFGGMF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AGFRFWPPFFPRRSQAGSSKFPT
                                                  SKTPSESIVAISECHTLLSCKVQLLGSQ-----ESECPDSVQRDVLSGGRHTH-----
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4.4%; Score 167; DB 7; Length 1596;
Best Local Similarity 19.8%; Pred. No. 0.58;
Matches 151; Conservative 112; Mismatches 286; Indels 214;
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
JETTICE OF INVESTION:
TITLE OF INVESTION: TWOR SUPPRESSOR GENE
FILE REFERENCE: A30558-A-FWC-A-A 070156.0597
CURRENT APPLICATION NUMBER: US/11/060,005
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 09/902,432
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1996-06-18
PRIOR FILING DATE: 1996-06-18
PRIOR FILING DATE: 1996-04-19
PRIOR PRILING DATE: 1996-04-19
PRIOR PRILING DATE: 1996-04-19
PRIOR FILING DATE: 1996-04-19
SEQ ID NOS: 35
SOFTWARE: FRASERQ for Windows Version 4.0
                                                                                                                                                                                  590 EHRERMFNRLQGTCFKGLNVLKQ 712
                                                                                                                                                                                                                541 AARARANARLRNPPLAPIPALTO 563
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ORGANISM: Rattus norvegicus
382 EDKEDDSEAALGEAES
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OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by OTHER INFORMATION: eMATRIX, accession number PF00632C, p-value=3.302e-23, raw score OTHER INFORMATION: 20.66
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OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: PFam, accession name HECT, E-value=4.3e-127, PFam score of 435.6
                                                                                                                                                                   -----OVTEEBAATAOKEEPSTLPNNVPAQE 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 FGGMF--PTRWLDFA---GVYSALRAL--KGREKPAAPTAQKSLSSLQLDSSDPSVTSPL 140
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350 AGDIPGNTQESTEEKIELLTTEVPLALBEESPSEGCPSSEIPMEKEPGEGRISVVDYSYL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1044 TGSKALEKVEEVEEDSEVLASEKEKDVMPKGPVQEAGAEHLAQGSETGQATPESLEVPEV
                                                                                                                              410 EGDLPISARPACS----NKLIDYILGGASSDLETSSDPEG------EDWDEEAEDDGFD
                                                                                                                                                                                                                                                                                                                                                                                      510 SEKDLSGKSDLENSSQ---SGSLPETPEHSSGEED--DW---ESSADEAESLKLWNSFCN
                                                                                                                                                                                                                                                                                                                                                                                                                          SDDPYNPLNFKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPD
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                                                                                                                                                                                                                                                       SDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIOTAARIVPEEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyeer, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REPERENCE: 790CTP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT APPLICATION NUMBER: US/10/6831

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR PILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 SVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEE 664
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; Sequence 57852, Application US/10450763
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      1162 ŚODŚKATAAVRÓS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1524).
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INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by INFORMATION: PFam, accession name HECT, E-value=5.5e-80, PFam score of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GMPFNPDPYLKISIQPGKHSIPPALPHHGQER-----RSKIIG------NTVNPI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 FGGMF--PTRWLDFA---GVYSALRAL--KGREKPAAPTAQKSLSSLQLDSSDPSVTSPL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LRASVKRKSRP-CSLPVSELETVIASACGDPETPRTHYIRIHTLLHSMPSAQGGSAAE 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWLEEGIHWQYSPPD-LKLELKAKGSALDPAAQAF------LLEQQLWGVELLPSS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEIHHLRMKRLEFLOOANKG-ODLPTPDODNGYHSLBEBHSLLRMDPKHCRDNPTQFVPA 349
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                                                                                                                                                                                                                                                                                                                                              ----SSPSGPLNIQRIDNFSVVSYLLNPSYLDC
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                                                                                                                                                                                                                                                                                                             31 AGSSKFPTP-LGPENSGNPTLLSSAQPETRVSYWT-KLLSQLLAPLPGL-LQKVLIWSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGRRLPTDHVSGQLQPRFEITSSIHPDDEEISLSTEPESAQIQD--SPMNNLMESGSGE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GEAPASTKEEPLE--EEATTQSRAGREEEEKEQEEEGDVST----LEQGEGRLQ-
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                                                                                                                                                                                                                                                             235;
                                                                                                                                                                                                            Length 1702;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                 = X or * as defined in Table
                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                             99; Mismatches 277;
                                                                                                                                                                                                          4.2%; Score 160.5; 20.9%; Pred. No. 1.4
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NU
TITLE OF INVENTION: BUCODING HUMAN ENG
TITLE OF INVENTION: USES THEREOF
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                                                                                                                                                                                                                                       Best Local Similarity 20.9%
Matches 161; Conservative
                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1702)
CTHER INFORMATION: Xaa
US-10-450-763-38864
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US-10-990-328A-9765
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OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: eMATRIX, accession number PF00632B, p-value=3.700e-21, raw score,
OTHER INFORMATION: 18.45
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-WQAEQFSFVSLPTDVLEIEVKDKFAKSRPIIKRFLGKLSMPVQRLLERHAIGDRVVSYT
                                                     SSPSGPLNIQRIDNFSVVSYLLNPSYLDC
                                                                                      PPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGL
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POL-
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLISCOM
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EEDGAEEESTLKDS---SEKDGL----
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LOCATION: (1257)..(1628)
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ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
LOCATION: (1470).
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                     NUCLEIC ACID
EXPRESSION OF 10,000
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1 Similarity 20.4%; Pred. No. 7.5;
93; Conservative 56; Mismatches 159;
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              TITLE OF INVENTION: DETECTION KIT, SUCH AS IN TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILL REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 1090-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR PELIGATION NUMBER: 60/160,191
PRIOR PELIGATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-03-24
                  DETECTION KIT, SUCH AS ARRAYS, FOR DETECTING
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Best Local Similarity
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LENGTH: 5303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 AGDIPGNTQESTEEKIELLTTEVPLALEE---ESPSEGCPSSEIPMEKEPGEGRISVVDY 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYLEGDLPISARPACSNKL--IDYILGGASSDLET------SSDPEGEDWDEEA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLSGKSDLENSSQSGSLPET--PEHSSG------EEDDWESSADEAESLKLWNSF 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 ------SPROGGDHSCEGC-DASCCSPSCYS-SSCYS-TSCYSSSCYSASCYS 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AGSSKFPTP-LGPENSGNPTLLSSAQPETRVSYWT-KLLSQLLAPLPGL-LOKVLIWSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PESTNGAGPWODELAAPSGHVERSPEGLESPVA-----GPSNRREGEC 781
                                                                                                                                                                                                                        Query Match
4.2%; Score 158.5; DB 6; Length 1585;
Best Local Similarity 20.9%; Pred. No. 1.7;
Matches 161; Conservative 99; Mismatches 277; Indels 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 PDSVQRDVLSGGR---HTHVKRKKVTFLEEVTEYYISGDEDRK----
                CURRENT APPLICATION NUMBER: US/10/990,328A CURRENT FILING DATE: 2004-11-17 NUMBER OF SEQ ID NOS: 558824 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 9765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOSRLYSNRELG------
FILE REFERENCE: CL001495
                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-10-990-328A-9765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-11-097-143-30390
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------TDGSSSADQVQQP-----QRIDEQETGEEXDGVGQAENDA 4783
607 CKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFA
                                                                                                                                                                                                                                                                                                               ; Sequence 31983, Application US/11097143; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     , APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                             US-11-097-143-31983
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; Sequence 30390, Application US/11097143

APPLICANT: Venter, J. Craig

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1906 APVDSDEDTSAPSDEKIPSVSGEEVEGPEVTTASPQAAEEDELKTPAESEPS----- 1957
                                                                 ---EDETKADETP-ESVTOVSDVATSTSAPV 1997
                                         561 NSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKV
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                                                                                                                                                                                     Sequence 62, Application US/10877346 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgess, Catherine E
                                                                                                                                                                                                                                                   MacDougall, John I
Smithson, Glennda
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                                                          Ellerman, Karen
Grosse, William M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-877-346-62
                                                                                                                                                                                                                                                                                                                                                                                                                       Lepley, Denise M
                                                                      -STDKVPETEYQKP
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| SSEEDENSSTDQIPSEVPEKKPETPAQ-TPEEGDIVGATAAPTTSDEVPPVQRLPEEVLA 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1758 EIPQPSTETGIKQQDETTAAPSIDRKEPYVTEIDEEATTVAPISEKDEKPTEEEKPVEQK 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPSAE------VEKEASGETSESDNEIDAGASSTPVPVSADEDKTPSTEKTVEADD 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1522 KFTTVAPLAGDEEESNLPKLPQDIFEEEAPVAVTTAAPSKDDGEQKPVEVEKPIEDGQK 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTAQKSL-----SSLQLDSSDPSVTS-PLDWLEEGIHWQYSPPDLKLELKAKGSAL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPAAQAFILLEQQLWGVELLPSSLQSRLYSNRELGSS-------PSGPLNIQRID 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EVSYQNSDGNSE 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 VVGFQTLTPESSCLREDHCHPQPLSAELIPASWQ-----GCPPLSTEGLPEIHHLRMK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       506 EPSDSEKDLSGKSDLENSSQSGSLPETPE----HSSGEEDDWESSADEAESLKLWNSFC 560
                 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.2%; Score 15%; DB 7; Length 276%;
21.4%; Pred. No. 3.6;
tive 62; Mismatches 226; Indels 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSLEEEHSLLRMDPKHC----RDNPTQFVPAAGDIPGNT-----
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PRIOR APPLICATION NUMBER: 60/15/,832

PRIOR APPLICATION NUMBER: 60/15/,832

PRIOR APPLICATION NUMBER: 60/16/,191

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/16/,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1999-11-28

PRIOR PILING DATE: 1999-11-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/194,831

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PRAECED FOR WINDOWS VERSION 4.0
                                                                                                CURRENT APPLICATION NUMBER: US/11/097,143 CURRENT FILING DATE: 2005-04-04
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Best Local Similarity 21.49
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: DROSOPHILA US-11-097-143-31983
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LENGTH: 2768
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                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 05/09/964,956

PRIOR PILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/235,633

PRIOR PILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: 60/236,064

PRIOR APPLICATION NUMBER: 60/236,064

PRIOR APPLICATION NUMBER: 60/236,065

PRIOR APPLICATION NUMBER: 60/236,065

PRIOR APPLICATION NUMBER: 60/236,066

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-28

PRIOR PLING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/236,135

PRIOR APPLICATION NUMBER: 60/237,434

PRIOR APPLICATION NUMBER: 60/239,321

PRIOR APPLICATION NUMBER: 60/239,321

PRIOR APPLICATION NUMBER: 60/239,321

PRIOR APPLICATION NUMBER: 60/239,231

PRIOR APPLICATION NUMBER: 60/239,231

PRIOR APPLICATION NUMBER: 60/230,230

PRIOR APPLICATION NUMBER: 60/230

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Best Local Similarity 19.1%; Pred. No. 4.1;
Matches 171; Conservative 105; Mismatches 261; Indels 360; Gaps
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
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33;

243;

Mismatches 249; Indels

82;

Conservative

147;

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Matches
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1852 ADQEEPKN------TAGDTPKPPQCVPESKPPQAA-------LGSLR 1885
                                                       1451 FHEDSISLSGPGGSSEPSP--SSMYGNAEDSSS----DPESLAEDPGAAARNNWSPPLSP 1504
                                                                                                                                                                                                                                                                              1612 GIMDVTSTSSNMGDSQSSQMTRHCRNAPFVLGNPDMVNDLGRDLLDEGAPKEGAAAASVM 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                              1342 PENPVTDIDNFIEEA-----SEARLSQSPQKADCRAHGDTFESQPPGGAGSSSSH- 1391
                                                                                                                                                                                                                                                                                                                                           1552 RAVCKPVGDICERACFVPGASRTSIPDSSQPFSFLDVSSEEPETWASINASQNHMPVCTE 1611
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1792 COKPKCSPKLKRLNSKGKASPEVPVALSTKGSRNDHRKTLPSPQASHKMFSKAVSHRLHI 1851
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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: CANCER
FILE REFREENCE: DFN -059-2
CURRENT APPLICATION NUMBER: PCT/USO5/18850
CURRENT PILING DATE: 2006-05-7
NUMBER OF SEQ ID NOS: 1528
SOFTHARE: PSESSEQ for Windows Version 4.0
LENGTH: 1503
                                      178 QQ------LWGVEL-LPSSLQ------SRLYSNRELGSSPSGPLNIQR---- 212
                                                                                           213 -----IDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHC 265
                                                                                                                                                 266 HPQPLSAELIPA----SWQGCPP----LSTEGLPEIH---HLRMKRLEFLQQANK---- 309
                                                                                                                                                                                                        ------GQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNP-----TQFVP 348
                                                                                                                                                                                                                                                            AAGDIPGNTQESTEEKIELLTTEVPLALEESPSEGCPSSEI------PMEK 394
                                                                                                                                                                                                                                                                                                                   E-----PGEGRISVVDYSYLEGDLDISAR-------PACSN 423
                                                                                                                                                                                                                                                                                                                                                                        424 KLIDYI-----LGGASSDLETS-----SDPE-----GED-WDEEAEDDGF----- 457
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ORGANISM: Homo sapiens
PCT-US05-18850-797
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DB 1; Length 1503;

Score 156.5; [Pred. No. 2.1;

4.1%;

Query Match Best Local Similarity

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963 GLVSALSSDSTSQDS-LLEDSLSAPPPASEPSLETPDSLESVDVHEALLDSLGSHTPQKL 1021
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                                                                                                                                        ELLSTDARTHSLD------DILAS 910
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                                     PRRVP-----DDSLPTQGETQPTCLDVIVPB-----DCLHQDISP----DAVTVPV 867
                                                                                                     86 QLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEE 145
                                                                                                                                                                                                         GIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPS 205
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                                                                                                                                                                                                                                                                                                                                                                                                                  -----WGFQTLTPESSCLREDHCHPQPL-SAELIPAS-----WQGCPP-----LSTE
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APPLICANT: Raelson, John V
APPLICANT: Bradley, Walter E
APPLICANT: Paquin, Bruno
APPLICANT: Nguyen-Huu, Quynh
APPLICANT: Croteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Little, Randall D
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Eerdewegh, Paul V
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                                                                                                                                                                  4.1%; Score 156; DB 8; Length 757;
19.8%; Pred. No. 0.95;
ative 90; Mismatches 218; Indels 170;
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                                                                                                                                                                                                                                                                       77 PGTLPST----PVTSF----PGIPDTLPPGSAPLEAPMTPVTDDSPQ-
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NUMBER OF SEQ ID NOS: 2738
SOFTWARE: Patentin version 3.3
SEQ ID NO 466
LENGTH: 757
TVDE: 757
TVDE: 77
                                                                                                                                                                  Query Match
Best Local Similarity 19.8
Matches 118; Conservative
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-60-685-372-466
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                                                                                                                                                                                                                                   40 WPLLMWQLLWLLVKEAQPLEWVKDPLQLTSNPLGP--PEPWSSHSSHFP-----RESP
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                                                                                                                                64; Mismatches 209; Indels 176;
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                                                                                Length 888;
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GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR PILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSTOM
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9
                                                                             Score 156; DB
Pred. No. 1.2;
                                                                                4.1%;
                                                                                                                                   Matches 134; Conservative
; ORGANISM: Homo sapiens
US-10-450-763-44262
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; OTHER INFORMATION: WW domain identified by PFam, accession name WW, E-value=7.6e; OTHER INFORMATION: -26, PFam score of 99.3 US-10-450-763-38863
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APPLICANT: Buck Institute
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OTHER INFORMATION: WW/rsp5/WWP domain proteins domain identified by eMATRIX, OTHER INFORMATION: accession number BL01159, p-value=8.568e-11, raw score of
                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 EVTVSPECHQTHHLDSPSVSVKPPDVQLTIAAEPSAEVGTSLVQQEATTRLSGSGNDIE 468
                                                   63 WTKLLSQLL-----APLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKP 115
                                                                                                                                                                             LDPAAQAFLLEQQLWGVELLPSSLQSRL-YSNRELGSSPSGPLNIQRIDNFSVVSYLLNP 225
                                                                                                                                                                                                 -----SYLD-----CFPRLEVSYQNSDGNSEVVG-----FQTLTPE---- 256
                                                                                                                                                                                                                                                                                                                                       252 QSSSLQQEAPAQLPQLLEEEPSSMQQEAPALPPESS--------MESLTLPWHEV 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPAIQHG-------GPPLLSESSEAGPLAVQQETSFQSPEPINNENPSPTQQE 515
                                                                                                                116 AAPTAOKSLSSLOLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLE----LKAKGSA--- 166
                                                                                                                                              HAPTL--PADPWDFDHLGPSASSEMP-----APPQESTENLVPFLDTWDSAGELP 138
                                                                                                                                                                                                                                                                         192 QSQKQTLQNEYSSTDTPYPGSLPPELRVKSDEPPGPSEQVGPSQFHLEPETQNPETLEDI 251
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                                                                                40 WPLLMWOLLWLLVKEAQPLEWVKDPLQLTSNPLGP--PEPWSSHSSHFP-----RESP 90
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(GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
ITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTHARE: CUSTOM
SEQ ID NO 38863
LEGGTH: 1391
   23.0%; Pred. No. 1.2;
ive 64; Mismatches 209; Indels
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                     Matches 134; Conservative
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NAME/KEY: DOMAIN
LOCATION: (705)..(989)
    Best Local Similarity
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                                                                                                                                                                           171 BEAAVITEAGDQGWYSYGPBGAGEL------LAQVQKDIQPAPSAEELAEQLDLGE
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                                                                                                                                                                                                                                                                         SSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGF-------T
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                                                                     Indels 255;
   Length 1391;
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Rang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Taylon, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465PC
Query Match
4.0%; Score 150.5; DB 6;
Best Local Similarity 19.8%; Pred. No. 4.1;
Matches 137; Conservative 87; Mismatches 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 NMDEDGFFEGELMDGRRGLVPSNFVERVSDDDLLTSLPPELADLSHSSGPELS--FLSVG 748
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                                                                                                                                                                                                                                                          21 WPPFFPRRSQAGSSKFPTPLGP----ENSGN-PTLLSSAQPETRVSYWTKLLSQLLAP 73
                                                                                                                                                                                Query Match
3.9%; Score 149; DB 1; Length 1857;
Best Local Similarity 20.7%; Pred. No. 7;
Matches 167; Conservative 80; Mismatches 254; Indels 304; Gaps
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CURRENT APPLICATION NUMBER: PCT/US03/10870
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3025
NUMBER OF FattSEQ for Windows Version 4.0
SEQ ID NO 2173
LENGTH: 1857
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                                                                                                                                                                                                                                                                                                                                74 LPGLLQKV-----
                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-2173
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Search completed: September 16, 2005, 10:56:21 Job time : 88.4089 secs

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                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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probable transcription factor SMAP - human N;Alternate names: skeletal muscle abundant protein C;Species: Homo sapiens (man) C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004 C;Accession: S68142
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C;Speciese: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10001
C;Accession: S10001
A;Iord, K.A.; Hoffman-Liebermann, B.; Liebermann, D.A.
Nucleic Acids Res. 18, 2823, 1990
A;Title: Sequence of MyD116 cDNA: a novel myeloid differentiation primary response gene
A;Reference number: S10001; MUD: 90251472; PMID: 2339071
A;Reference mRNA
A;Ressidues: 1-657 <LOR>
A;Residues: 1-657 <LOR>
A;Residues: 1-657 <LOR>
A;Cross-references: UNIPROT: P17564; EMBL: X51829; NID: 953040; PIDN: CAA36128.1; PID: 953041
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A36535

A36535

add34 protein - long-tailed hamster
MyAlternate names: MyD116 protein homolog
G;Species: Criceculus long-tailed hamster)
G;Species: Criceculus long-taudatus (long-tailed hamster)
G;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
G;Accession: A56535
R;Zhan, Q.; Lord, K.A.; Alamo Jr., I.; Hollander, M.C.; Carrier, F.; Ron, D.; Kohn, K.W.
Mol. Cell. Biol. 14, 2361-2371, 1994
MyTitle: The gadd and MyD genes define a novel set of mammalian genes encoding acidic procession: A56535
A;Reference number: A56535
A;Reference number: A56535
A;Reture presiminary
A;Residues: 1-590 <ZHA>
A;Residues: 1-500 <ZHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 KRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNP-----TQFVP--- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPGLQSADKSLGEVVAGEEGVTE------1AY-PTSHWEGCPSEEEBDGETVKKA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRASADSPGHKSSTSVYCPGEAEHQATEEKQTENKADPPSSPS------GSHSRAW 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 WVYRPGEDTEDDDDSDWGSAEEEGKALSSPTSPEHDFLKAWVYRPGEDTEDD--DDSDWG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSSOSG---SLPETPEHS-----LSGE--EDDWESSADEAES------L 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLSCKVQLLGSQES-----BCPDSVQRDVL-----SGGRHTHVKRKKVTFLEEVTEY 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFQVAFYLPGEKPAPPWTAPKLPLRLQRRLTLLRTPTQDQDPETPLRARKVHFSENVTVH 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----IPMEKE-----PGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPYNPQNFT------ATIQTAARIVPEEP------SDSEKDLSGKSDLE 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLWNSFCNSDDPYN-----PLNFKA--PFQTSGENEKGCRDSKTPSESIVAISEC-HT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETSSDPEGEDWDE-----EARDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSE-----
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FLAVWAGPAQAARRGPWEQLARDRSRFARRIAQAEEKLGPYLTPAFRARAWARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%; Score 201; DB 2; Length 590;
33.9%; Pred. No. 7.9e-05;
ve 56; Mismatches 210; Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.9%;
Matches 142; Conservative 5
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PIDN: AAB40884.1

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A;Cross-references: EMBL;L46815; NID:g1377885; PID:g1377886; PIDI
A;Experimental source: strain BALB/c; clone T1; thymocyte, brain
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPSADKSGLGLG 2064
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A;Status: preliminary
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  R;Nielsen, M.S.; Munck Petersen, C.; Gliemann, J.; Madsen, P.
Bjochim. Biophys. Acta 1306, 14-16, 1996
A;Title: Cloning and sequencing of a human cDNA encoding a putative transcription factor A;Tetle: Cloning and sequencing of a human cDNA encoding a putative transcription factor A;Accession: S68142
C;Status preliminary
A;Residues: 1-757
A;Accession: S68142
A;Cross-references: UNIRROT:Q15355; EMBL:X87613; NID:g1009425; PIDN:CAA60949.1; PID:g100
C;Superfamily: bromodomain homology
P;626-681/Domain: bromodomain homology
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T42717
T42717
T42717
DNA-binding protein Rc - mouse
NyAlternate names: lg kappa chain gene enhancer Recognition component
C;Spectes: Mus musculus (house mouse)
C;Spectes: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
R;Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, Z.; Yu, C.Y.
Genomics 35, 415-424, 1996
A;Title: The mouse DNA binding protein Rc for the kappa B motif of transcription ew family of large transcriptional proteins
A;Reference number: Z22238; MUID:97001141; PMID:8812474
A;Reference number: Ranscriptional proteins
A;Referenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 QDLDEELGSTAAGEILEADVAIGKGDETPLTNVKTEASPESML----SPSHGSNPIED-- 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLEGDLPISARPACSNKLIDYILGGASSDLETS-SDPEGEDWDEEAEDDGFDSDSSLSD- 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 QYSPPDIKLELKAKGSALDPAAQAFILEQQIMGVELLPSSLOSRLYSNRELGSSPSGPLN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVSQPDNCVPMEAVG---DPHTVTVSMDSS--EISMIINSIKEECFRS-GVAEAFVG--- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 IQRIDNFSVVSYLLNPSYLDCFPRLE--VSYQNSDGNSEVVGFQTLTPESSCLREDHC-- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 HPEVLDVAAVEAALSFCEENDDPQSLPG-PWEHPIQ-----QERDKPVPLPAPEMTVK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QDNGYHSL---EEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTE--- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EKI------BLLTTEVPLALEESP-----SEGCPSSEIPMEKEPGEGRISVVDYS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----WLDFAG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 -KKMLGQKATPPPSPLLSELLKK---GSLLPTSPRLVNESEMAVASGHLNSTGVLLEVGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PLEARTQHKFEMSDSLKEESGTIFGSQIKDAPGED----EEEDGVSEAASLEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTLPST----PVTSP----PGIPDTLPPGSAPLEAPMTPVTDDSPQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 HPQPLSAELIPASWQGC----PPLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEEDOGEGYLSEMDNEPPVSE-----SDDGFSIHNATLOSHTLADSIPSSPASSO 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGTGGSRKRLGPRAGPRFWPPFFPRRSQAGSSKPPTPLGPENSGNPTLLSSAQPETRVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAARIVPEEPSDSE 511
                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 159; DB 2; Length 757;
20.0%; Pred. No. 0.044;
ive 89; Mismatches 218; Indels 170;
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A;Molecule type: mRNA
A;Residues: 1-2282 <WUL>
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.0
Matches 119; Conservative
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146444 hypochetical protein DKFZp434N1427.1 - human hypochetical protein DKFZp434N1427.1 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C;Accession: T46444 styleoceker, H.; Boecher, M.; Boecher, M.; Boecher, M.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LK---KHIRTH-TDVRPYVCKHCHFAFKTKGNLTKHMKSKAHSKKCQETGVLEELEAEEG 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1884 ISEATHLTASSCSTPSRGTQGLPRLGLAPLEKDMSSAP----SPKATSPRRPWSPSKEA 1938
                                                                                                                                                                                                                                                                                                                                                                                                          1456 OGRSRREAET----LSSLSSDVSDPKELSPLSHSTLSHGTAPGSEALKEYAQPSSKAHRR 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLPPMSVKKEDPKEQTDLPPLPPLAPPSSL--PLSDTSPKPAKLQEGTDSKKVL-QPPSLHTT 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1677 KQGKAEEG--TPTSKRGEPARVKIFEGGYKSNEEYIYVRGRGRGRYVCEECGIRCKKPSM 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1791 -TSDDLHQDSEGQEGAEAVEEHQF----------SDLEDSDS 1823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526
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                                                                                                                                                                                                                                                                      31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRMDPKHCRDNPTQFVP-----AAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 CPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDPE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 GEDWDEEAEDDGFDSDSSLS------474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: RC
C;Function:
A,Description: binds V(D)J recombination signal sequence and kappa B motif
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA recombination; transcription factor
                                                                                                                                                                                                                                                                                                                                             OMHI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 YSPP-DLKLELKAKGSALDPAAQAFILEQQLWGVELLPSSLQSRLYSNRELGSSPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GPLNIQRIDNFSVV----SYLLNPSYLDCFPRLEVSYQNSDGNSEVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEI-----HHLRMKRLE
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                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                      213;
                                                                                                                                                                                                   Length 2282;
                                                                                                                                                                                                                                                                      Indele
                                                                                                                                                                                                   Query Match
4.0%; Score 150.5; DB 2;
Best Local Similarity 22.5%; Pred. No. 0.67;
Matches 151; Conservative 64; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                          110 KGREKPAAPTAQKSLSSLQLDSSDPSVTSPL--DWLEEG
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PLFNMNAMSALYHIAQNESPVLQSGHWSEYFRNFVDSCLQKIPQDRPTSE-----VLLK 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEIPMEKEPGE-----GRISVVDYSYLEGDLPISARPACS--NKLIDYILGGASSDLET 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 QPEITPSPLQPPAAPAPTSTTSSARRRAYCRNRDHFATIRTASLVSRQIQEHEQDSALRE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQ--ET 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :| : | : | : | : | : | 404 ----QENPSTPKREKAEWILKQKEQILQCCQA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSGKSDLENSSQSGSLP-----ETPEHSSGEEDDWESS----ADEAESLKLWNSFCN 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPD 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 ------QQHILGQQKKEL--ARAAQAEERKF-------QQHILGQQKKEL-- 403
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S58225
R;Nielsen, M.S.
Rshitted to the EMBL Data Library, May 1995
A;Reference number: S58225
A;Accession: S58225
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-647 <NIE>
                                                                                                                                                                                                                                                                                    LNPSRLSSIP------STREET
                                                                                                                                                                                                                                          223 LNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGC
                                                                                                                                                                                                                                                                                                                             PPLSTEGLPEIHHLRMKRLEFLQQANKG-------QDLPTPDQDNGYHSLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSV------DPY
                                                                                                                                                                                                   Gaps
                                                                                                                                                  3.9%; Score 150; DB 2; Length 1062;
20.5%; Pred. No. 0.25;
ive 71; Mismatches 187; Indels 192;
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3.9%; Score 149; DB 2; Length 647;
Best Local Similarity 20.5%; Pred. No. 0.15;
Matches 123; Conservative 86; Mismatches 213; Indels 178;
A;Molecule type: mRNA
A;Residues: 1-1062 <AAA>
A;Residues: 1-1062 <AAA>
A;Cross-references: UNIPROT:Q9NSW2; EMBL:AL137701
A;Cross-references: dult testis; clone DKFZp434N1427
C;Genetics:
A;Note: DKFZp434N1427.1
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C;Superfamily: bromodomain homology
C;Keywords: skeletal muscle
F;506-561/Domain: bromodomain homology <BR02>
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                                                                                                                                                Query Match 3.9%
Best Local Similarity 20.5%
Matches 116; Conservative
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Gaps

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C;Accession: T03730
R;Fisher, L.W.; Merrelli, A.; Benayahu, D.
submitted to the EMBL Data Library, July 1997
A;Description: Clone containing epitope to mouse osteoblast monoclonal antibody MMS-85/1
A;Reference number: Z15035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AjStatus: preliminary; translated from GB/EMBL/DDBJ
Abdlecule type: mRNA
AjResidues: 1-1567 <FIS>
AjCross-references: UNIPROT:035243; EMBL:AF013969; NID:g2384710; PIDN:AAB69856.1; PID:g2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 GKGDETPLTNVKTEASPESML----SPSHGSNPIED------PLEAETQHKFEMSDSL 439
                                                                                                                                                                               96 -WLDFAGVYSALRALKGREKP----AAPTAQ--KSLSSLQLDSSDPSVTSPLDWLEEGIH 148
                                                                                                                                                                                                                                                                  60 VLLEVGGVLPMIHGGEIQQTPNTVAASPAASGAPTLSRL-LEAGPTQFTTPL---ASFT 114
                                                                                                                                                                                                                                                                                                                                                         149 WQYSPPDLKLELKAKGSALDPAAQAFILEQQLWGVELLPSSLQSRLYSNRELGSSPSGPL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 NIQRID-----PRIMSVILINPSYLLOCF------PRLE---- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :: | :| :| :| STATE | STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 EKMDIAVSYTGEELDFETVG-----DIIAIIEDKVDDHPEVLDVAAVEAALSFCEENDD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 PQSLPG-PWEHPIQ-----QERDKPVPLPAPEMTVKQERLDFEETENKGIHELVDIRE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 ALEEESP----SEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYI 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 LGGASSDLETS-SDPEGEDWDEEAEDDGFDSDSSLSD-----SDLEQDPEGLHL 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SDDGFSIHNATLQSHTLADSIPSSPASSQLPMDLSTIKKNIEN----GLIRSTAE 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGLPE-IHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQF 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 VPAAGDIPGNTQESTEEKIELLTTEVPLALEEE-----SPSEGC-----PSSEIPMEK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VSYQNSDGNSEVVGFQTLTPESSCLREDHC--HPQPLSABLIPASWQGC----P 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPD------QDNGYHSL---EE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTE-----EKI-----ELLTTEVPL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 KEESGTIFGSQIKDAPGED----EEEDGVSEAASLEEPKEEDQGEGYLSEMDNEPPVSE- 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 WNSFCSVDPYNPQNFTATIQTAARIVPEEPSDSE--KDLSG-KSDLENSSOSGSLPETPE 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen containing epitope to monoclonal antibody MMS-85/12 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                  3 PVIDDSPOKKMLGOKATPPPSPLLSELLKK---GSLLPTSPRLVNESEMAVASGHLNSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 YONSDGNSEVVGFQTLTPESSCLREDH-----CHPQPLSAEL---IPASWQGCPPLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 134;
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56 PETRVSYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 105; Conserv
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		671 QY 533 PEHSSGEEDDWESSADEAESLKLWNSFCNSDDFYNPLNFKAPFOGGENEKGCR	587 DSKTPSESIVAI	RESULT 9 R.B.; Garner, C.C. C;Species; Ms musculus (knuse mouse) C;Date: 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T17202 R;Van Slouw, P. P.H.; Romeijn, R.J.; Eeken, J.C.J. Mutat. Res. 433, 109-116, 1999 A;Title: Molecular cloning, expression and chromosomal localisation of the mouse Rev31 gf A;Accession: T17202 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Roleculer type: mRNA A;Residues: 1-3122 <van> A;Coss-references: UNIPROT:Q61493; EMBL:AF083464; NID:g4079831; PIDN:AAC98 A;Experimental source: strain 129/Ola; testis</van>	A; Reduction: 10 C; Reywords: nucleotidyltransferase A; Cross-references: EMBL: X66840 A; Cross-references: EMBL: X66840 C; Superfamily: microtubule-associated protein C; Superfamily: microtubule binding; phosphoprotein C; Reywords: microtubule binding; phosphoprotein	Length 2774; Qy 70 LLAPLPGLLQKVLIWSQLFGGMPPTRWLDFAGVYSA 105	109	ELKAKGSALDPAAQAFLLEQQIWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRID 214	NFSVVSYLLNPSYLDCFPPLAIGRIDNFSVVSYLLNPSY 227 SCHLAPVSIPEPHRATVSPSTDETPAGTLPGGSFSHSALSVDRKHSPGEITGPGGHFMTS 1294 OY 187PSSLQSRLYSNRELGSSPSGPLAIGRIDNFSVVSYLLNPSY 227 SCHLAPVSIPEPHRATVSPSTDETPAGTLFRWEEDEIPSSLLLEGVEPLSTCELEVDAVA 242	ESSCIREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRWKRLEFLQQANKGQD 312 QY 228 LDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCIREDHCHPQPLSAELIPASWQG 281
PACSNKLIDYILGGAS. -CCGRKGSTEALSGCS	DWESSAL : RDEFSS: TPSESIV ::	VKKKVTFLEEVTEYYISGDI :- :- :: SNKEIANLEEKSTSNI		4 - rat / rat) ion 31-Dec-1993 #text_chi iller, R.; Vallee, R.B.; 22 23 25629; PMID:1379599 GB:M83196; NID:G205537; I backbone (NCBIN:111039) June 1992	-751, 5, 'W',	ength 2	LEEGII - KEQQPI	LYSNR! QFGEL!	LEVSYQN :: LSVDRKH	EIHHL!

282 CPPLSTEGLPEIHHLRMKRL-EFLQQANKGQDLP-TPDQDNGYHSLEEEHSLLRMDP	338 HCRDNPTQEVPAAGDIPGNTQESTEEKIELLTTE-VPLALEESSPSEGCPSSE358 YV-DGPVVF-PSHIDDEIIQLPDYEDSPIVLPIETEIEGSESSESSDSE
Qy 337 KHCRDNPTQFVPAAGDIPGNTQBSTBEKIELLTTEVPLALEBESPSEGCPSSEIPME 393 1 :	Qy 390IPMEKEPGEGRISVVDXSYLEGDLPISARPACSNKLIDYILGGAS 434
QY 394 KEPGEGRISVUDYSYLEGDLPISARPACSNKLIDYILGGASSDLE 438	QY 435 SDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSV 484 :::
Qy 439 TSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQN 491 : :	OY 485 DPYNPQNFTATIOTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSSGEEDD 542
492 FTATIGTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPETPEHSGGEDDWESSADEAE 479EHCAKKRSLCRNAHRSTEEDD-SSSEERE	RESULT 11 A82255
552 SLKLWNSPCDS	hypothetical protein VC0998 [imported] - Vibrio cholerae (strain N16961 serogroup O1) C; Species: Vibrio cholerae C; Date: 18 Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C; Accession: A82255
Qy 589 KTPSESIVALSECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVT 642	R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I. R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
Qy 643 PLREVT 648 : Db 615 PTKRST 620	A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A.Reference number: A82035; MUID:20406833; PMID:10952301 A.Accession: A82255 A.Status: preliminary
RESULT 10 837762 225K protein - Babesia bovis (fragment) C;Species: Babesia bovis C;Date: 19-May-1994 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004	A,Molecule type: DNA A,Resicues: 1-1621 (AEL) A,Resicues: 1-1621 (AEL) A,Cross-references: UNIPROT:Q9KTA5, GB:AE004181; GB:AE003852; NID:g9655454; PIDN:AAF9415- A,Experimental source: serogroup O1; strain N16961; biotype E1 Tor C,Genetics: A,Gene: VC0998 A,Gene: VC0998
C;Accession: S37762 R;Jasmer, D.P.; Reduker, D.W.; Perryman, L.E.; McGuire, T.C. Mol. Biochem. Parasitol. 52, 263-270, 1992 A;Title: A Babesia bovis 225-kilodalton protein located on the cytoplasmic side of the e A;Reference number: S37762; MUID:92319010; PMID:1377786	Query Match 3.7%; Score 142.5; DB 2; Length 1621; Best Local Similarity 20.5%; Pred. No. 1.3; Matches 155; Conservative 100; Mismatches 278; Indels 223; Gaps 35;
A;Accession: S37762 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-574 c/AS>	QY 33 SSKPTPLGPENSGNPTLLSSAQPETRVSYWTKLLSQLLAPLPGL 77 1::
ferences: UNIPROT:Q00708; EMBL:M80466;	78 LQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDFSVT
Query Match 3.8%; Score 143.5; DB 2; Length 574; Best Local Similarity 20.3%; Pred. No. 0.27; Matches 109; Conservative 78; Mismatches 194; Indels 157; Gaps 25;	Db 837
57 ETRVSYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPA : :: : : : :	861 EPLTLNDLELPEENDEPQLAEVTPSSAFDEQQVETEIEPESEPLAAEASNDESDLTALNE
DD 136 KVKIRHYNRLYPGLLQQLPDYLLEKALKCNIYEGISPDVMLEIEYYLKVKNRWKFM 191 QY 117 APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDP 169 : : :	QY 172QAFLLEQQLWWVELLESSLQSKELGSSFSGFLNIQKLUNFSVVSILLMFSIL 228 :
Db 192 SPEIIRDINDENMDTNDSKRAQVIPTIPSPSITDE 226 Ov 170 AAOAFIJEOOLWGVRIJPSSIASRIASRIASSPSGPINIORIDNFSVVSVIJNDSVID 229	QY 229 DCFPRLEVSYQNSDGNSBVVGFQTLTPESSCLREDHCHPQPLSABLIPASWQGCPPLSTE 288
227 VIQYEBSYDGPVVFPSHIDDEIIQLPDYEBSPIVLP	289 GLPEIHHIRMIKRLEFLOQANKGODLPTEDQDNGYHSLEEEHSLLRMD-PKHCRD
Qy 230 CFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSABLIPA 277	3LDLP
Qy 278 SWQGCPPLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPK 337 	DD 1068 DALADSQLEPAAESEVEPELELVSEPVTEEAFTELDELDLPEYTEEDALADAQ 1120 Qy 376 LEBESPSECCPSSEIPMEKEPGEGRISVVDY-SYLEGDLPISARPACSNKLIDY 428

Qy 629 SGGRHTHVKRKKVTFLEEVTEYISGDEDRKGPW 662 : : :: : : : Db 1402 GATQDVPPTQSLANKAFDEEALHDWLSDNPDGEKPF 1437	T22139 hypothetical protein F43G6.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T22139; T22174 R;Swinburne, J.
SAB170 SRP40 protein - yeast (Saccharomyces cerevisiae) SRP40 protein - yeast (Saccharomyces cerevisiae) Nylternate names: protein YKR092c; protein YKR412a C;Species: Saccharomyces cerevisiae C;Date:: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: 338170; 3340645; 33702 Submitted to the Protein Sequence Database, March 1994 A;Reference number: 338158 A;Accession: S38170 A;Molegule type: DNA	
A; KeBidues: 1-406 cBAL> A; KeBidues: 1-406 cBAL> A; KeBidues: 1-406 cBAL> A; Cross-references: UNIPROT: P32583; EMBL: Z28317; NID: 9486580; PID: 9486581; MIPS: YKR092c A; Experimental source: strain S288C R; Bou, G.; Esteban, P.P.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji Yeast 9, 1349-1354, 1993 A; Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromc A; Reference number: S40644; MUID: 94205265; PMID: 8154186 A; Accession: S40645 A; Molecule type: DNA	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Reaidues: 1-83 < 472> A;Rolecule type: DNA A;Reaidues: 1-83 < 472> A;Cross-references: EMBL:283108; PIDN:CABO5512.1; GSPDB:GN00020; CESP:F43G6.9 A;Experimental source: clone F44E5 C;Genetics: A;Gene: CESP:F43G6.9 A;Map position: 2 A;Introns: 21/1; 68/3; 122/3; 186/3; 381/3; 474/3; 641/2; 752/3
A;Cross-treferences: EMBL:X73541; NID:g450550; PIDN:CAA51946.1; PID:g450552 A;Experimental source: strain S288C R;tallo, D; Caxles, C.; Senfenac, A.; Thuriaux, P. submitted to the EMBL Data Library, May 1993	Query Match 3.7%; Score 141.5; DB 2; Length 833; Best Local Similarity 18.1%; Pred. No. 0.6; Matches 139; Conservative 106; Mismatches 251; Indels 273; Gaps 36;
A;Description: Interactions between three common subunits of yeast RNA polym A;Reference number: 837702 A;Accession: 837702 A;Molecule type: DNA	t and Qy 6 GGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGN Db 50 GGGLDNIGENAELENYATQTAKLRFDDPVWQKPSSSDHVAPSASEIPIPFPNFGNGDA
A;Residues: 1-399,'N',401-406 <lal> A;Cross-references: EMBL:L11275; NID:g295670; PID:g295671 C;Genetics: A;Genetics: A;Genes: SGD:SRP40 A;Gene: SGD:SRP40 A;Cross-references: SGD:S0001800; MIPS:YKR092c A;Map position: 11R</lal>	Qy 48PTLLSSAQPETRVSYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDF 108 SDSFKSSFEAESFFLKKSIWGNGTDGAYNIWGTNFGISSVPAAPTLDLDF Qy 100 AGVYSALRALKGREKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGI
Query Match 3.7%; Score 142; DB 2; Length 406; Best Local Similarity 23.4%; Pred. No. 0.21; Matches 71; Conservative 27; Mismatches 121; Indels 84; Gaps	DD 158 GALLPIFILIGATKEVASSQIPSMPSSALTLEBUCEKMQMGNKFUSLVUAFKULUGUGSTFVQ 217 QY 148HWQYSPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPS 205 10;
Qy 310 TEVPLALEESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDY1 4	429 QY 191 Db
QY 430 LGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNP 4 :	489 QY 264 HCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKRL

Qy 302 BFLQQANKGQDLPTPDQDNGYHSLBEBHSLLRWDPKHCRDNP 343	QY 549 EAESLKIWNSFCNSDDPYNPLNPKAPFQTSGENEKGCRDSKTPSESIVA 597 280 SEISDSYMSYSDGPGTSMPIRPIRTGTPDGTWGDCTWCFEVPIEPQGCNRCQQIIG 335
QY 344 TQFV-PAAGDIPGNTQESTEEKIELLTTEVPLALEEESPEGCPSSEIPMEKEPGEGRIS 402	Qy 598 ISECHTLLSCKVQLLGSQESECPDSVQRDVLSGG 631
QY 403 VVDY-SYLEGDLPISARPACSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDG 456 Db 440 FAGYMSYKEREWLIRIQFIQCKGSGDPQVDDYYYVTWRDKQIANG 484 QY 457 FDSDSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAARIVPEEPSDSEKDLSG 516	RESULT 15 A57376 probable regulatory protein 322 - rat C;Species: Rattus norvegicus (Norway rat)
Db 485 WTAETKLEEATKEK	C.Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 08-Feb-1996 C;Accession: A57376 E;Accession: A57376 E;Accession: A57376 E;Lin, X.; Nelson, F.J.; Frankfort, B.; Tombler, E.; Johnson, R.; Gelman, I.H. Nol. Cell. Biol. 15, 2754-2762, 1995 A;Fitle: Isolation and characterization of a novel mitogenic regulatory gene, 322, which A;Reference number: A57376; MJD:95257957; PMID:3739556
559 FCNSDDPYNPLNFKAPPQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGS ::: :: ::: ::: :: :: :: ::	A,Accession: A57376 A,Status: preliminary; not compared with conceptual translation A,Molecule type: mRNA A,Residues: 1-1346 <lin> A,Residues: 1-1346 <lin> A,Cross-references: GB:U23146</lin></lin>
dy 615gesechsvo-kovskokkkyirlesvitäyisgde 656	C;Genetics: A;Gene: 322 Query Match 3.7%; Score 139; DB 2; Length 1346; Best Local Similarity 19.6%; Pred. NO. 1.7; Matches 145. Concervative 112. Mismatches 246. Indels 188. Gans 34.
φι	4 GTGGSRKRLGPRAGPRFWPPFFPRSQAGSKFPTPLGPENSGNPTLLSSAQPETRV
1	
A,Accession: T25234 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-846 <wil></wil>	OY 107 RALKGREKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKG 164
	Qy 165 SALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYL 222 :
108/2; 258/2; 338/2; 369/3; 3	QY 223 INPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQ 268
Query Maccn 3.7%; Score 139; DB 2; Length 846; Best Local Similarity 21.8%; Pred. No. 0.88; Matches 87; Conservative 44; Mismatches 160; Indels 108; Gaps 13;	
QY 305 QQANKGQDLPTPDQDNGYHSLEEBHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQE 359	Db 561 VDFTSEAVTAT-ETSEALRTEEVTEASGAB-ETTDMVSAVSQLTDSPDTTEEATPVQEVE 618 Qy 320 NGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKIELLTTE 371
OY 360 STERKIELLTTEVPLALEESPSECCPSSEIPMEKEPGEGRISVV 404	Db 619 GGVLDTEEERRQTQAILQAVADKVKEESQVPATQTVQRTGSKALEKVEBVEEDSEVLASE 678 Ov 372 VPLALREESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLID 427
405 DYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDD 132 VESDDEFISETTIDERESSEPRESSDFHHFTD-FREDDSNMDDRESSCONS	679 KEKDVMPKGPVQBAGABHLAQGSETGQATPESLEVPEVTADVDHVATCQVIKLQQLME 428 VILGGASSDLETSSDPEGEDWDEREAEDDGPDSDSSLSDSDLEODPEGLHLWNS
456	: : : : : : : : : : : :
191 SPNSAAAVASHTGPTLRRSNNSRSSGFRPESBSIIMDELTINDE	Qy 481 FCSVDPYNPQNFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGS 528 : : :
OY 489 FORFIATIOIAAKI VEEFFOUSEKUUSGASULKANSQASALKEI FERSSONEEDIMESSAN 348 	529 LPETPEHSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEK

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ò	584 GCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTF 643
q	874 KAADVTYDSE-VMGVAGCQEKEŠTEVĢSLSEBGEMETDVEKEKRETK 920
à	644 LEEVTEYYISGDEDRKGPWEE 664
Q	921 PEGVSEEGEQETAAPEHE 938

Search completed: September 16, 2005, 10:46:36 Job time : 25.1914 secs

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ALIGNMENTS

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Nat. Genet. 36:40-45(2004).
EMBL; AK027650; BAB55266.1; -.
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B. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Romastein M.J., Usdin T.B., Toobliyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Gardan A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garder B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC065280; AAH652280.1; --
SEQUENCE 713 AA, 79125 WW; 76C2DA38F9E76A85 CRC64;
                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein phosphatase 1, regulatory subunit 15B.
Name-PPPIRI5B;
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RR SEQUENCE FROW N.A.

RA MARGAMETOL J. 10198/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA MARGAMETOL A., Hayashi K., Saro H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

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RA Marakami K., Yasuda T., Isono Y., Nakamura Y., Nagahari K.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Shigawara M.,

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RA Takahashi M., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Minomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,

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RA Woshikawa Y., Matsunawa H., Ichhara T., Shiohata N., Sano S.,

Noriya S., Komiyama H., Satoh N., Takami S., Terashima Y., Wakebe H.,

RA Massakino K., Yukit H., Obihma A., Takemoto M., Kawakami B.,

RA Masayawa S., Senoh A., Mizoguchi H., Goto Y., Shinizu F., Wakebe H.,

RA Amazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami T.,

RUJimori Y., Xomiyama M., Tashiro H., Tanigami A., Fuliwara T.,

RA Masabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

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RA Matanama M., Hata H., Watanabe M., Komatsu T.,

RA Matanama M., Matanabe T., Nowura N., Kikuchi H., Masuho Y., Yamashita R.,

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Homo sapiens (Human).
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                                                                                                                                                                                                              WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDDFSVVSYLLNPSYLDCFPRLEVSYQN 240
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                                                                                                                                   SYWTKLLSQLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKGREKPAAPTA 120
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
                                                                                                                                                                                                                                                                                                                                                                                    CSNKLIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNS
                                                                                    MEPGTGGSRKRLGPRAGFRFWPPFPPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV
                                                                                                                                                                                                                                                                                    LEFLQQANKGQDLPTPDQDNGYHSLEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHTLLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKG
                                                                       1 MEPGTGGSRKRLGPRAGFRFWPPFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV
                                                                                                                                                                                                  WGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN
                                                                                                                                                                                                                                          SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR
                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                              Length 713;
                                                  Indels
        79125 MW; 26C2D06144AAD25E CRC64;
                                                  0
                             Score 3794; DB 2;
Pred. No. 1.5e-201;
                                                  2; Mismatches
                             99.78;
Genew; HGNC:14951; PPP1R15B
                                                  Matches 711; Conservative
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           713 AA;
                                         Similarity
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C STRAIN=C5'BL/6J; TISSUE=Cerebellum, and Spinal cord;
X MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Isashiro H., Itoh M.,
A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Nomeda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/61; TISSUE=Cerebellum, and Spinal cord; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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SEQUENCE FROM N.A.
STRAIN=557BL/6J; TISSUE=Cerebellum, and Spinal cord;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Spinal cord;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE-2TOROM Consortium;
"FIXEN PANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Cerebellum, and Spinal cord;
The FANTOM Consortium,
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
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                                              G0:000164; C:protein phosphatase type 1 complex; IDA. G0:0000164; C:protein phosphatase type 1 complex; IDA. G0:0004722; F:protein serind-threonine phosphatase activity; G0:0004722; F:protein serind-crackity; IC. G0:000583; F:R-overload response; IDA. G0:0006484; P:regulation of translational initiation; IC. G0:0006494; P:response to hydrogen peroxide; IMP. G0:0006779; P:response to oxidative stress; IDA.
                                                                                                                                                                                                                           17;
                                                                                                                                                                                              Query Match 63.6%; Score 2419.5; DB 2; Length 697; Best Local Similarity 68.9%; Pred. No. 1.4e-125; Matches 482; Conservative 54; Mismatches 147; Indels 17;
Hayashizaki
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashi:
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AK049028; BAC33517.1; -
EMBL; AK082957; BAC38708.1; -.
                                                                                                                                                                     77711 MW; E439B12615F33737 CRC64;
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                                                  RESULT 4
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Q658M2 PRELIMINARY; PRT; Q658M2; 25-OCT-2004 (TrEMBLrel. 28, Created)

0658M2 ID 06 AC 06

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CKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFA 666
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                        Fobo
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                           Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
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The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQGTCFKGLNVLKQC
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                                                                                                                                                                                                                                                                                      Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB833746; CAH56240.1; -.
Hypothetical protein.
I
                                                                                                                                                                                                                                                                                                                                                                                                                              407 AA; 45218 MW; FSAFFAEF48BB3704 CRC64;
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
Hypothetical protein DKFZp666I186 (Fragment).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.2%; Score 2177; DB 2; Best Local Similarity 99.8%; Pred. No. 1.7e-112; Matches 406; Conservative 1; Mismatches 0;
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                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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909

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366

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120 486 180 546 240

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(Fragment).
Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M.J., Uddin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A., Rathery J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Jones S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAAQAFLLEQQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR 300
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                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058078; AAH58078.1;
GO; GO: 0000164; C: protein phosphatase type 1 complex; IDA.
GO; GO: 0004722; F: protein serine/threonine phosphatase activity; IDA.
GO; GO: 000645182; F: translation regulator activity; IC.
GO; GO: 0006993; P: RER. overload response; IDA.
GO; GO: 0006446; P: regulation of translational initiation; IC.
GO; GO: 00042542; P: response to hydrogen peroxide; IMP.
GO; GO: 0006579; P: response to oxidative stress; IDA.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
llbrary, clone:D930040107 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.8%; Score 1285; DB 2; Length 408; 63.5%; Pred. No. 3.5e-63; ive 37; Mismatches 100; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45432 MW; 44AA70EPE25796C4 CRC64;
                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                 cDNA sequences."
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GTRAIN-GSBL/63; TISSUE-Head;
Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Haraka H., Hashizume W., Hangabil T., Haraka T., Haraka T., Hirozane T., Rukuda S., Furuno M., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katch H., Kawai J., Kojima Y., Konno H., Konno H., Kouda M., Koya S., Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Sano H., Saitoh H., Saitoh H., Sakazume N., Sanzume N., Sano H., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (ApR-2002) to the EmBL/GenBank/DDBJ databases.

R EMBL, AKO8660; BAC39701.1; -.
R MGD, MGI:2444211; Ppplr15b.
R MGO; GO:0000164; Ciprotein phosphatase type 1 complex; IDA.
GO; GO:0004722; F:protein phosphatase type 1 complex; IDA.
GO; GO:0004722; F:protein serine/threonine phosphatase activity; IDA.
GO; GO:0006493; P:Eranslation regulator activity; IC.
R GO; GO:000646; P:regulation of translational initiation; IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                         STRAIN=CS7BL/60; TISSUE=Head; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayabhizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/64); TISSUB-Head;
Shibata K., TISOM M.,
Shibata K., Magaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Sumi N., Itohi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matumunoto H., Sakaguchi S., Indegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahika M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                             RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/60; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
                    Name=Ppp1r15b;
Mus musculus (Mouse)
                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                      NCBI_TaxID=10090;
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227 YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 WPGEDTEEE-EDEEEDEDSDSGSDEEEGEAEASSSTPATGVFLKSW-----VYQPGED 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDPAAQAFILLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 FVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSEI------PMEKEPG 397
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                         SVQRDVLSGGRHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQETED 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 HRECCPAVE---EEDD------EEAVKKEAHRTSTSALSPGSKPSTWVSCP-- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SSGEEDDWESSADBAESLKLWNSFCNSDDPYNPLNFKAPFQTSG-----ENEKG 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 FADGQRAPL----SPSILIRTLQGSDKNPGEEKAEEEGVAEEEGVNKFS----YPPS
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 LLAPLPGLLOKVLIWSOLFGGMFPTR-WLDFAGVYSAL--RALKGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L1
SQUENCE FROM N.A.
Ebert L., Schick M., Neubert P., Schatten R., Henze S., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR457259, CAG33540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 EGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDLETSSDP-
                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 265.5; DB 2; ilarity 21.9%; Pred. No. 1.5e-06; Conservative 81; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP-
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                                                                                                                                                                           135 IIEFCLSENHRRNIKTHLK 153
                                                                                                                                                                                                                                                                                                                         061A96;
05-7UL-2004 (TrEMBLrel. 27, C
05-7UL-2004 (TrEMBLrel. 27, L
05-7UL-2004 (TrEMBLrel. 27, L
PPPIRISA procein.
Name-PPPIRISA;
Homo sapieng (Human).
                                                                                                                         682 AIGYCLTFEHRERMFNRLQ
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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hes 164;
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                                                                                                                                                                                                                                                                                                                                                                                RYWTKLLSQLLALLPSLFQKLLLWSQLFGGLIPTRWLDFAASYSALRALRGREESAAPTV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKGELKAKGSALDPAAQAFLLEQQL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGVELLPSSLOSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCFPRLEVSYQN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLPEIHHLRMKR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHTLLSCKVQLLGSQESECPD 621
                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 QEKADVKKDMSLVDDNGVENKELS-KLSETDSFQEMDESDEDSSNDTDTENMELMNMPCR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                  1 MEPGTGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPETRV
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
CNPV31 MyD116-like domain protein.
Name=CNPV231;
Canarypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                  16;
                                                                                                                                              Match 32.6%; Score 1241; DB 2; Length 376; Local Similarity 65.1%; Pred. No. 8.4e-61; les 255; Conservative 35; Mismatches 86; Indels 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Tulman B.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F.,
"The genome of canarypox virus.";
J. Virol. 78.353-366(2004).
EMBL; AY318871; AAR83577.1; -.
SRQUENCE 158 AA; 18892 MW; FEE7CDF3E79642IC CRC64;
                                                                                               972525D3D472C8F8 CRC64;
GO:0042542; P:response to hydrogen peroxide; IMP GO:0006979; P:response to oxidative stress; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEEKIELLTTEVPLALEESPSEGCPSSEIPM 392
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                                                                                             376 AA; 41949 MW;
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GO; GO:0042542; P:resp
GO; GO:0006979; P:resp
Hypothetical protein.
NON TER 376
SEQUENCE 376 AA; 41
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NCBI_TaxID=44088;
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                                                                                                                                              Query Match
                                                                                                                                                                                               Matches
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066VZB6
1006VZB6
2000
AC 06VZ
DD 05-J
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32; 112

182

259

443

Š 셤 δ 셤 32;

Gaps

80; Mismatches 263; Indels

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Matches 164; Conservative
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaunar R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B. Stapleton M. J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
B. Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
F. Generation and initial analysis of more than 15,000 full-length human
                                                                        AEDWGEAEPCPFRVAI -----YVPGEKPPPPWAPPRLPLRLQRRLKRPETPTHD 544
                                                                                                                                                          545 PDPETPLKARKVRFSEKVIVHFLAVWAGPAQAARQGPWEQLARDRSRPARRIIQAQEELS 604
                                                                                                                            -----VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFOKRIQETEDAIG
                        CRD--SKTPSESIVAISECHTLLSCKVQLLGSQ-----ESECPDSVQRDVLSGGRHTH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97298078; PubMed=9153226; DOI=10.1074/jbc.272.21.13731; Hollander M.C., Zhan Q., Bae I., Fornace A.J. Jr.; Mammalian GADD34, an apoptosis- and DNA damage-inducible gene."; J. Biol. Chem. 272:1313-13737(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Apoptosis a ssociated protein (Protein phosphatase 1, regulatory subunit 15A).
Name=GADD34; Synonyms=PPP1R15A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 260.5; DB 2; Length 674;
21.9%; Pred. No. 2.8e-06;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                             YCLTFEHRERMFNRLQGTCFKGLNVLKQ 712
                                                                                                                                                                                                                                                                                PCLTPAARARAWARLRNPPLAPIPALTO 632
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                     | : |: |: |: |: || RPEEEAADSGGPGEDRETLGLKTSSSLPEAWGLLD-DDDGMYGEREATSVP---RGQGSQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDVDSEDKEDDSEAALGEAES-----DPHPSHP-DQRAHFRGWGYRPGKETEEEEB 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544
                                                                                                                                                                                                                                       ----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 LDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 YLDCFPRLEVSYONSDGNSEVVGPOTLTPESSCLREDH-CHPOPLSAELIPASWOGCPPL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 WEYRSG------BASEEKEEKAHKETGKGEAAPGPQSSAPAQRPQLKSWWCQPSDEEG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 WPGEDTEER-EDEEEDEDSDSGSDEEEGEAEASSSTPATGVFLKSW------VYQPGED 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP------ETPEH-- 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-----EEEEEDEDSDTGSAEDEREAETSASTPPASAFLKAWVYRPGEDTEEEED 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SSGEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSG-----ENEKG 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GEEENQATEDKRTERSKGARK-----TSVSPRSGGDPRS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLAPLPGLLQKVLIWSQLFGGMFPTR-WLDFAGVYSAL--RALKGR------
                                                                                                          LLSPVMGLLSRA--WSRL-RGLGPLEPWLVEAVKGAALVEAGLEGEARTPLAIPHTPWGR
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PubMed=14702039; DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Oteuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10499.
Homo sapiens (Human).
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Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sudawara M., Takahashi M., Kanda K., Yokoi T., Pruvya T., Kikkawa E., Omura Y., Abe K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanibashi T., Yamashita H., Murakawa K., Fujimori K., Anita M., Imose M., Manabhino K., Takahashi-Fujii A., Hara H., Tanase T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Anehori K., Takahashino K., Yuuki H., Oshima A., Sasaki N., Anta M., Imose N., Musabhino K., Yuuki H., Oshima A., Sasaki N., Anta M., Imose N., Makagawa S., Senoh A., Ichihara T., Shiohata N., Sano S., Nomiyama H., Satoh N., Takami S., Terashima Y., Sano H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Amazaki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y., Amazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Matsumura K., Nakajima Y., Miranuo T., Shakai M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Antahama K., Nakajima Y., Maranabe T., Shirai Y., Takahashi Y., Nakagawa K., Matsuhura K., Nakajima Y., Maranabe T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura N., Isogai T., Sugano S., Nakai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Wana K., Nakai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S., Makai M., Makai K., Yada T., Nakagima Y., Ohara O., Isogai T., Sug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 -----EKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSA 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 LDPAAQAFILLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDH-CHPQPLSAELIPASWQGCPPL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNPTQ 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EGEDWDEEAEDDGFDSDSSLSDSDLEQDPEG-----LHLWNSFCSVDPYNPQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 VYWPGEDTEEE-EDEEEDEDSGSDEEEGEAEASSSTPATGVFLKSW-----VYQPG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 NFTATIQTAARIVPEEPSDSEKDLSGKSDLENSSQSGSLP-------ETPEH 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | : | : | : | : | : | EDT-------EBEBDBDSDTGSAEDEREAETSASTPPASAFLKAWVYRPGBDTEBE 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRECCPAVE---EEDD------EEAVKKEAHRTSTSALSPGSKPSTWVSCP-- 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 36:40-45(2004).
EMBL; AK001361; BAA91649.1; -.
SEQUENCE 674 AA; 73363 MW; 8F988E873B29CBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 166; Conservative
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                                  635
                                                                                                                    547 PETPLKARKVRFSEKVTVHFILAVWAGPAQAARQGPWEQLARDRSRFARRIAQAQEELSPC 606
--DPHP----SHPDQSAHFRGWGYRPGK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWLDFAGVYSALRALKG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 REKPAAPTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQYSPPDLKLELKAKGSALDPAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 QAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRIDNFSVVSYLLNPSYLDCF 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
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                                                                  ETEEEEAAEDWGEAEPCPFRVA--IYVPGEKPPPPWAPPRLPLRLORLKRPETPTHDPD
                                                                                                    ----VKRKKVTFLEEVTEYYIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIGYC
                                  590 TPSESIVA----ISECHTLLSCKVQLLGSQ-----ESECPDSVQRDVLSGGRHTH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lord K.A., Hoffman-Liebermann B., Liebermann D.A.;
"Sequence of MyD116 cDNA: a novel myeloid differentiation primary
response gene induced by ILG.";
Nucleic Acids Res. 18:2823-2823(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 233; Indels 292;
                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myeloid differentiation primary response protein MyDll6.
Name=Mydl16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AALLTPTPVSG-NLLP-----HGETEESGSPEOSOAAORL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (incomplete).
9B217001019C38A7 CRC64;
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PIR; S10001; S10001.
MGD; MGI:1100516; Myd116.
Antiqen; Differentiation; Repeat.
Antiqen; Differentiation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 237; DB 1; 21.8%; Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                           657 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                      LIFEHRERMFNRLQGTCFKGLNVLKQ 712
                                                                                                                                                                                                       LTPAARARAWARLRNPPLAPIPALTO 632
 EDEDVDSEDKEDDSEAALGEAES----
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MEDLINE-90251472; PubMed-2339071;
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Best Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 KAWVYRPGEDTEEEDDGDWDSAEEDASQSCTTPHTSAFLKAWVYRPGEDTEEEDDSENVA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 PVDSETV----DSCOSTQHCLPV-----EKTKGCGEAEPPPFQVAFYLPGQKPAP 427
                                  ------WGL 108
                                                                                                        ---PLHLQ 143
                                                                                                                                                                                                                 272 AELIPAS-WOGCP---PLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEE 327
                                                                                                                                                                                                                                                                                         EHSLLRMDPKHCRDNPTQFVPAAGDIPGNTQESTEEKI------ELLTTEVPLALE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAWVYRPGEDTEEE-----TSAFL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausher R.D., Collina F.S., Wanger L. Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Browstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Broasak S.A., McDewn P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                      SPPDLKLELKAKGSALDPAAQAFLLEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQ
                                                                                                                                            212 RIDNFSVVSYLLNPSYLDCFPRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLS
                                                                                                                                                                                                                                                                                                                           ------KPSTSVYCPGBAEHRATEBKGTDNKAEPSGSHSRVWEYHTRERPKQEG
---YSALRALKGREKPA-APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQY
                                                                                                                                                                               ---YPTSHWEGGPAEDEEDTETVKKAH------QASAASIAP-----GY----
                                                                                                                                                                                                                                                                                                                                                                 EESPSEGCPSSEIPMEKEPGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPET-----PEHSSGEEDDWESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-BABSLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIV-----
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIS-----GDEDRKGPWEEFARDGCRFOKRIQETEDAIGYCLTFEHRERMFNRLQ 700
                                61 LLTPPPVSENHLPLRETEGNGTPEWSKAAQRLCLDVEAQSSPPKT---
                                                                                                        SDID---EHNGK-----PGODGLREQEVEHTAGLP-TLQ--
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Name=Myd116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWL--DFAGV----- 102
                                                                                                        ------KRLGEVVAREEGVAEPAYPTSQLEGGPAENEEDGETVKTYQASAASIAPGYKP 198
                                                                                                                                                                                  STPVPFLGEA-----EHQATEEK----GTE-NKADPSNSPSSGSHSRAWEYYSREKPKQ 247
                                                                                                                                                                                                                      GRISVVDYSYLEGDLPISARPA----CSNKLID-------YILGGAS 434
                                                                                                                                                                                                                                                                                               ---GEDWDEEAEDDGFDSDSSLSDSDL 468
                                                                                                                                                                                                                                                                                                                                                                   -----ATIQTAARI---VPEEP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 PWAAPKLPLRLQRRLRLFKAPTRDQDPEIP------LKARKVHFAEKVTVH 558
   PRLEVSYQNSDGNSEVVGFQTLTPESSCLREDHCHPQPLSAELIPASWQGCPPLSTEGLP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SPRPQ-HVLHWKEAHSFYLLSPLMGFLSRA--WSRLRGPEVSEAWLAETVAGANQIEADA 60
                                                                          BIHHLRMKRLEFLQQANKG---ODLPTPDQDNGYHSLEEEHSLLR------MDPKHCR
                                                                                                                                            DNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSS--EIPMEKEPGE
                                                                                                                                                                                                                                                         ------EGEAKVEAHRAGOGHPCRNAEAEEGGPETTFVCTGNAFLKAWVYRPGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SADEAESLKLWNSFC-----NSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSES
                                    VEAESSPPETWGLSNVDBYNA-KPGQDDLREKEMERTAGKATLQPAGLQGAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIS-----GDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTFEHRERMFNRLQ 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 217; DB 2; Length 578;
; Pred. No. 0.00058;
80; Mismatches 225; Indels 258;
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MEDIINE-22697643; Physical 128135; DOI=10.1038/sj.onc.1206567;
MPOILMR-22697643; Physical S., Fornace A.J. Jr.;
"Gadd34 functional domains involved in growth suppression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orcegene 22:3827-3832(2003).
EMBL; AY128642; AAM77795.1; -.
SEQUENCE 578 AA; 63569 MW; 923EC49921C0BC61 CRC64;
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Name=Gadd34;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YSALRALKGREKPA-APTAQKSLSSLQLDSSDPSVTSPLDWLEEGIHWQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----WGI 108
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywhinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                53 SAQPETRVSYWTKLLS-QLLAPLPGLLQKVLIWSQLFGGMFPTRWL--DFAGV-----
                                                                                                                                                                                                                                                                                                                                                                                                    | :|: | :| :| | ||:|| | | : | ||:| | 4 SPRPQ-HVLHWKEAHSFYLLSPLMGFLSRA--WSRLRGPEVSEAWLAETVAGANQIEADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AELIPAS-WQGCP---PLSTEGLPEIHHLRMKRLEFLQQANKGQDLPTPDQDNGYHSLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KPSTSVYCPGRAEHRATEEKGTDNKAEPSGSHSRVWEYHTRERPKQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --AISECHTLLSCKVQLL---GSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEEVTEY
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PLAVWAGPAQAARRGPWEQFARDRSRFARRIAQAEEQLGPYLTPAFRARAWTRLR 527
                                                                                                                                                                                                                                                                                                           5.6%; Score 214; DB 2; Length 578;
21.1%; Pred. No. 0.00085;
ative 81; Mismatches 225; Indels 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-EAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg R.;
Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC072513; AAH72513.1; -.
SEQUENCE 578 AA; 63583 MW; D9387CA71923345F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KVGEVVAREEGVSELA----
                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAARIVPEEPSDSEKDLSGKSDLENSSQSGSLPET----
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEVVGFQTLTPESSCLREDHCHPQPLSAEL----IPASWQGCPPLSTEGLPEIHHLRM 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEAERSGTPEEGKAAQGPCLDVQANSSPPETLGLSDDDKQGQDGPREQGRAHTAGLPILL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IPMEKE-----PGEGRISVVDYSYLEGDLPISARPACSNKLIDYILGGASSDL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --EAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSV 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 EYCSKQEGEADPEPHRAGKYQLCQNAEAEEEERAKVSSLSVSS------GNAFLKA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 SAEEEGKALSSPTSPEHDFLKAWVYRPGEDTEDDQDSDWGSAEKDGLAQTFATPHTSAFL 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLMGF--LSRAWSRLRVPEA-PEPWPAETVTGADQIEADAHPAPPL----VPE-NHPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPGLOSADKSLGEVVAGEEGVTE-----LAY-PTSHWEGCPSEEEDGETVKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRLEFLQQANKGODLPTPDQDNGYHSLEEEHSLLRMDPKHCRDNP-----TQFVP---
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23.9%; Pred. No. 0.0046;
rative 56; Mismatches 210; Indels 186; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        Ron
                                                                                                                                                                                       Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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Flavwagpaqaarrgpweqlardrsrfarriaqaeeklgpyltpafrarawarl
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                                                                                                                                                                                                                                                                                                                                                                                                                     Carrier F.,
                                                                                                                                                                                                                                                                                                                                                                                                               Zhan Q., Lord K.A., Alamo I.Jr., Hollander M.C., Carrier F., Kohn K.W., Hoffman B., Liebermann D.A., Fornace A.J.Jr., in the gadd and MyD genes define a novel set of mammalian genes acidic proteins that synergistically suppress cell growth."; Mol. Cell. Biol. 14:2361-2371(1994).

EMBL, L28147, AAA5983.1; -.

SEQUENCE 590 AA; 64527 MW; B3DB79BDACBAEGD6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 FRASADSPGHKSSTSVYCPGEAEHQATEEKQTENKADPPSSPS-
                                                                              Last sequence update)
Last annotation update)
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                                                       Created)
PRT;
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PRELIMINARY;
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01-JUN-2003 (TrEMBLrel.
Gadd34 protein.
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Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10030;
                       060465;
01-NOV-1996
                                                                                                                                                                Name=Gadd34;
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Q9VTN2;
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Q9VTN2
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Addman M.D. (Calniker S. B., Holt R. A., Fabran C. A., Gocapur J.D.,

RAMAMARIA (Calniker S. B., Holt R. A., Earns C. A., Gocapur J.D.,

RAMAMARIA (Calniker S. B., Holt R. A., Earns C. A., Gocapur J.D.,

RAMAMARIA (Ges P. G., Scherer S. B., Li P. W. Hoskins R. A., Galle R. F.,

Sutton G. G., Wortman J. R., Yandlell M.D., Zhang Q., Chen L. X.,

RAMAMARIA (S. ROGER Y. H., Blazel R.G., Champe M., Ffelifer B.D.,

RAMAMARIA J. F., Agbayani A., An H.J., Andrews Pfennkoch C., Baldwin D.,

RADILI J. F., Agbayani A., An H.J., Andrews Pfennkoch C., Baldwin D.,

Rallew R. M., Benso P. V., Berman B. P., Bardati D., Bolahakov S.,

Radeson K. Y., Benso P. V., Berman B. P., Bardati D., Bolahakov S.,

RAMAMARIA (S. R. Busam D. A., Bulke C. Davenport L. B., Davies P.,

Radelson K. J. Evaley S., Dahlke C. Davenport L. B., Davies P.,

Radelson K. J. Boule R. J., Downes M., Digan Rocha S., Punkov B. C., Dunn P.,

RAMAMARIA (Gabriellan A.E., Garzell J. H., Galbart W. Glasser K.,

Robin K. J., Evalesher R., Royland T. J., Wet M. M., Ibeyawa C.,

Raderin D., Houston K.A., Howland T. J., Wet M. M., Ibeyawa C.,

Allali M., Kalush F., Kalpen G. H., Kazi, Kalp D., Lai Z.,

Lasko P., Lei Y., Leviteky A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Leviteky A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntoeh T. C., McLeod M. P., Morbherson D.,

Raderiulov G., Milahina N. V., Mobarry C., Morris J., Moshreii A.,

Raderiulov G., Milahina N. V., Mobarry C., Morris J., Woshreii A.,

Rader E., Spradling A.C., Stapleton M., Stupaki M. P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Stupaki M. P., Smith H.O,,

Rader S. M., Worse S. W., Weinschond V., Warng S., Yao Q. A., Yeh R. R., Zhong F., Zhon M., Zhon S., Zhon W., Sanger B., Shu Wang Z. Y., Wasserman D.A., Weinschole S., Rober S., Smith H.O.,

Raden S. M., Woodager, Worley X.C., Wu D., Yang S., Yao Q. A., Yeh R. R., Zaveri J. S., Zhon W., Zhon S., Zhon S., Smith H.O.,

Raden S. M., Woodager, Worley X., Shu S., Shu S., Shu S., Shu S., Shu S., Shu S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
 Created)
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(TrEMBLrel. 13,
                -OCT-2002 (TrEMBLrel.
-OCT-2003 (TrEMBLrel.
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                                01-OCT-2003 (TrENCG6004-PB.
ORFNames=CG6004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877 STEGPLSTESSTEANESSSTESQDSTTQESSSSTEGPLSTESSTEGSNESSSTE--SS 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 ODSTIQESSSTESPLSTEANESSSTESQUSTIQESSSTEGPLSTESSTEANE 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 INPSYLDCPPRLEVSYQNSDGNSEVVGPQTLTPESSCLREDHCHPQPLSAELIPASWQGC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 PPLSTEGLPEIHHLRMKRLEFLQQANKGQDLP------TPDQDNGYHSLEEEHSL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SSTEGSNESSSTESSODSTTOESSSTESPLSTEPSTEANESSSTESSODSTTOESSS 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------KHCRDNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEESPSEGCPSSEIPMEKEP-----GEGRISVVDYSYLEGDLPISARPACSNK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 LEQQLWGVELLPSSLQSRLYSNRELGSSPSGPLNIQRI-------DNFSVVSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTQESSSS----TESPLSTEPSTEANESSSTESSODSTTQESSSSTEGPLSTEPSTEA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIDYILGGASSDLETSSDPEGEDWDEEAEDDGFDSDSSLSDSDLEQDPEGLHLWNSFCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPYNPQNFTATIQTAARIVPEEPSDSEKDLSGKSDLE--NSSQSGS-----LPETPEHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.6%; Score 174; DB 2; Length 1444;
21.4%; Pred. No. 0.45;
ative 71; Mismatches 222; Indels 122; Gaps
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                               Lewis S.E.; Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STPGNDDDSGNSGSENGNSSTSGSPCTTDNPSDP---ESSSSTPGNDD 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GEEDDWESSADEAESLKLWNSFCNSDDPYNPLNFKAPFQTSGENE 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0940; CHIT BIND II; 3.
SEQUENCE 1444 AA; 149406 MW; EFIC9643D693B3E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                            Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE003543; AAF50015.2; --
FlyBase; PBgn0036203; CG6004.
GO; 00000576; C:extracellular; IEA.
GO; GO:0000601; F:chitin binding; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
InterPro; IRR02557; Chitin_bind_PerA.
SPART; SM00494; ChEBD2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                   systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
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Search completed: September 16, 2005, 10:45:57

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